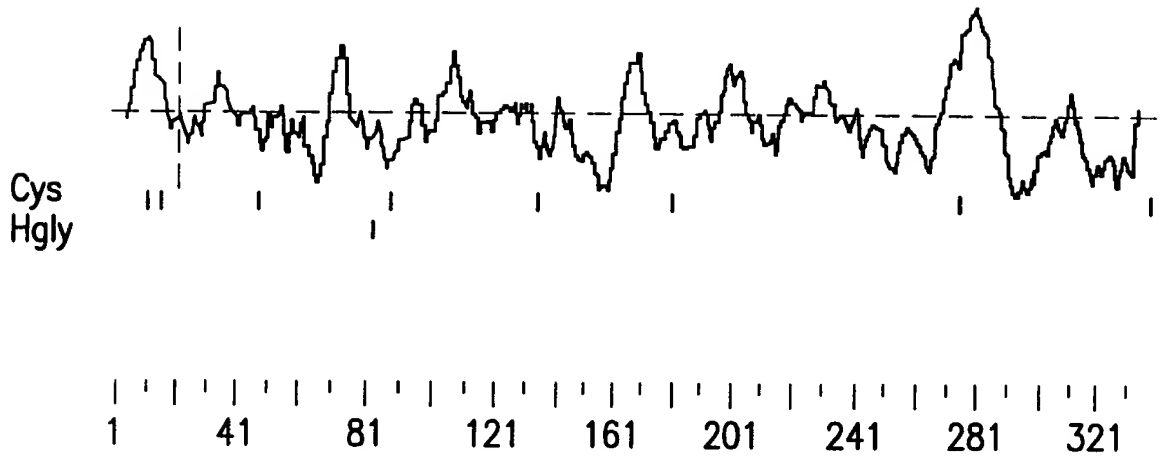
```
                                                  M  S  P  S  P  T  A  L  F  C  L    11
GGAGTCGACCCACGCGTCCGCAGGGCTGAGGAACC ATG TCT CCA TCC CCG ACC GCC CTC TTC TGT CTT    68

 G  L  C  L  G  R  V  P  A  Q  S  G  P  L  P  K  P  S  L  Q    31
GGG CTG TGT CTG GGG CGT GTG CCA GCG CAG AGT GGA CCG CTC CCC AAG CCC TCC CTC CAG   128

 A  L  P  S  S  L  V  P  L  E  K  P  V  T  L  R  C  Q  G  P    51
GCT CTG CCC AGC TCC CTG GTG CCC CTG GAG AAG CCA GTG ACC CTC CGG TGC CAG GGA CCT   188

 P  G  V  D  L  Y  R  L  E  K  L  S  S  S  R  Y  Q  D  Q  A    71
CCG GGC GTG GAC CTG TAC CGC CTG GAG AAG CTG AGT TCC AGC AGG TAC CAG GAT CAG GCA   248

 V  L  F  I  P  A  M  K  R  S  L  A  G  R  Y  R  C  S  Y  Q    91
GTC CTC TTC ATC CCG GCC ATG AAG AGA AGT CTG GCT GGA CGC TAC CGC TGC TCC TAC CAG   308

 N  G  S  L  W  S  L  P  S  D  Q  L  E  L  V  A  T  G  V  F   111
AAC GGA AGC CTC TGG TCC CTG CCC AGC GAC CAG CTG GAG CTC GTT GCC ACG GGA GTT TTT   368

 A  K  P  S  L  S  A  Q  P  G  P  A  V  S  S  G  G  D  V  T   131
GCC AAA CCC TCG CTC TCA GCC CAG CCC GGC CCG GCG GTG TCG TCA GGA GGG GAC GTA ACC   428

 L  Q  C  Q  T  R  Y  G  F  D  Q  F  A  L  Y  K  E  G  D  P   151
CTA CAG TGT CAG ACT CGG TAT GGC TTT GAC CAA TTT GCT CTG TAC AAG GAA GGG GAC CCT   488

 A  P  Y  K  N  P  E  R  W  Y  R  A  S  F  P  I  I  T  V  T   171
GCG CCC TAC AAG AAT CCC GAG AGA TGG TAC CGG GCT AGT TTC CCC ATC ATC ACG GTG ACC   548

 A  A  H  S  G  T  Y  R  C  Y  S  F  S  S  R  D  P  Y  L  W   191
GCC GCC CAC AGC GGA ACC TAC CGA TGC TAC AGC TTC TCC AGC AGG GAC CCA TAC CTG TGG   608

 S  A  P  S  D  P  L  E  L  V  V  T  G  T  S  V  T  P  S  R   211
TCG GCC CCC AGC GAC CCC CTG GAG CTT GTG GTC ACA GGA ACC TCT GTG ACC CCC AGC CGG   668

 L  P  T  E  P  P  S  S  V  A  E  F  S  E  A  T  A  E  L  T   231
TTA CCA ACA GAA CCA CCT TCC TCG GTA GCA GAA TTC TCA GAA GCC ACC GCT GAA CTG ACC   728

 V  S  F  T  N  K  V  F  T  T  E  T  S  R  S  I  T  T  S  P   251
GTC TCA TTC ACA AAC AAA GTC TTC ACA ACT GAG ACT TCT AGG AGT ATC ACC ACC AGT CCA   788

 K  E  S  D  S  P  A  G  P  A  R  Q  Y  Y  T  K  G  N  L  V   271
AAG GAG TCA GAC TCT CCA GCT GGT CCT GCC CGC CAG TAC TAC ACC AAG GGC AAC CTG GTC   848

 R  I  C  L  G  A  V  I  L  I  I  L  A  G  F  L  A  E  D  W   291
CGG ATA TGC CTC GGG GCT GTG ATC CTA ATA ATC CTG GCG GGG TTT CTG GCA GAG GAC TGG   908

 H  S  R  R  K  R  L  R  H  R  G  R  A  V  Q  R  P  L  P  P   311
CAC AGC CGG AGG AAG CGC CTG CGG CAC AGG GGC AGG GCT GTG CAG AGG CCG CTT CCG CCC   968
```

FIG.1A

```
 L  P  P  L  P  Q  T  R  K  S  H  G  G  Q  D  G  G  R  Q  D  331
CTG CCG CCC CTC CCG CAG ACC CGG AAA TCA CAC GGG GGT CAG GAT GGA GGC CGA CAG GAT 1028

 V  H  S  R  G  L  C  S  *                                    340
GTT CAC AGC CGC GGG TTA TGT TCA TGA                          1055

CCGCTGAACCCCAGGCACGGTCGTATCCAAGGGAGGGATCATGGCATGGGAGGCGACTCAAAGACTGGCGTGTGTGGAG 1134

CGTGGAAGCAGGAGGGCAGAGGCTACAGCTGTGGAAACGAGGCCATGCTGCCTCCTCCTGGTGTTCCATCAGGGAGCCG 1213

TTCGGCCAGTGTCTGTCTGTCTGTCTGCCTCTCTGTCTGAGGGCACCCTCCATTTGGGATGGAAGGAATCTGTGGAGAC 1292

CCCATCCTCCTCCCTGCACACTGTGGATGACATGGTACCCTGGCTGGACCACATACTGGCCTCTTTCTTCAACCTCTCT 1371

AATATGGGCTCCAGACGGATCTCTAAGGTTCCCAGCTCTCAGGGTTGACTCTGTTCCATCCTCTGTGCAAAATCCTCCT 1450

GTGCTTCCCTTTGGCCCTCTGTGCTCTTGTCTGGTTTTCCCCAGAAACTCTCACCCTCACTCCATCTCCCACTGCGGTC 1529

TAACAAATCTCCTTTCGTCTCTCAGAACGGGTCTTGCAGGCAGTTTGGGTATGTCATTCATTTTCCTTAGTGTAAAACT 1608

AGCACGTTGCCCGCTTCCCTTCACATTAGAAAACAAGATCAGCCTGTGCAACATGGTGAAACCTCATCTCTACCAACAA 1687

AACAAAAAAACACAAAAATTAGCCAGGTGTGGTGGTGCATCCCTATACTCCCAGCAACTCGGGGGGCTGAGGTGGGAGA 1766

ATGGCTTGAGCCTGGGAGGCAGAGGTTGCAGTGAGCTGAGATCACACCACTGCACTCTAGCTCGGGTGACGAAGCCTGA 1845

CCTTGTCTCAAAAAATACAGGGATGAATATGTCAATTACCCTGATTTGATCATAGCACGTTGTATACATGTACTGCAAT 1924

ATTGCTGTCCACCCCATAAATATGTACAATTATGTATACATTTTTAAAATCATAAAAATAAGATAATGAAAAAAAAAAA 2003

AAAAAAAAAAAAAAGGGCGGGCCGCTAGACTAGTCTAGAGAACA                 2047
```

FIG. 1B



MSPSPTALFCLGLCLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGPPGVDLYRLE
KLSSSRYQDQAVLFIPAMKRSLAGRYRCSYQNGSLWSLPSDQLELVATGVFAKPSLSAQP
GPAVSSGGDVTLQCQTRYGFDQFALYKEGDPAPYKNPERWYRASFPIITVTAAHSGTYRC
YSFSSRDPYLWSAPSDPLELVVTGTSVTPSRLPTEPPSSVAEFSEATAELTVSFTNKVFT
TETSRSITTSPKESDSPAGPARQYYTKGNLVRICLGAVILIILAGFLAEDWHSRRKRLRH
RGRAVQRPLPPLPPLPQTRKSHGGQDGGRQDVHSRGLCS

FIG.2

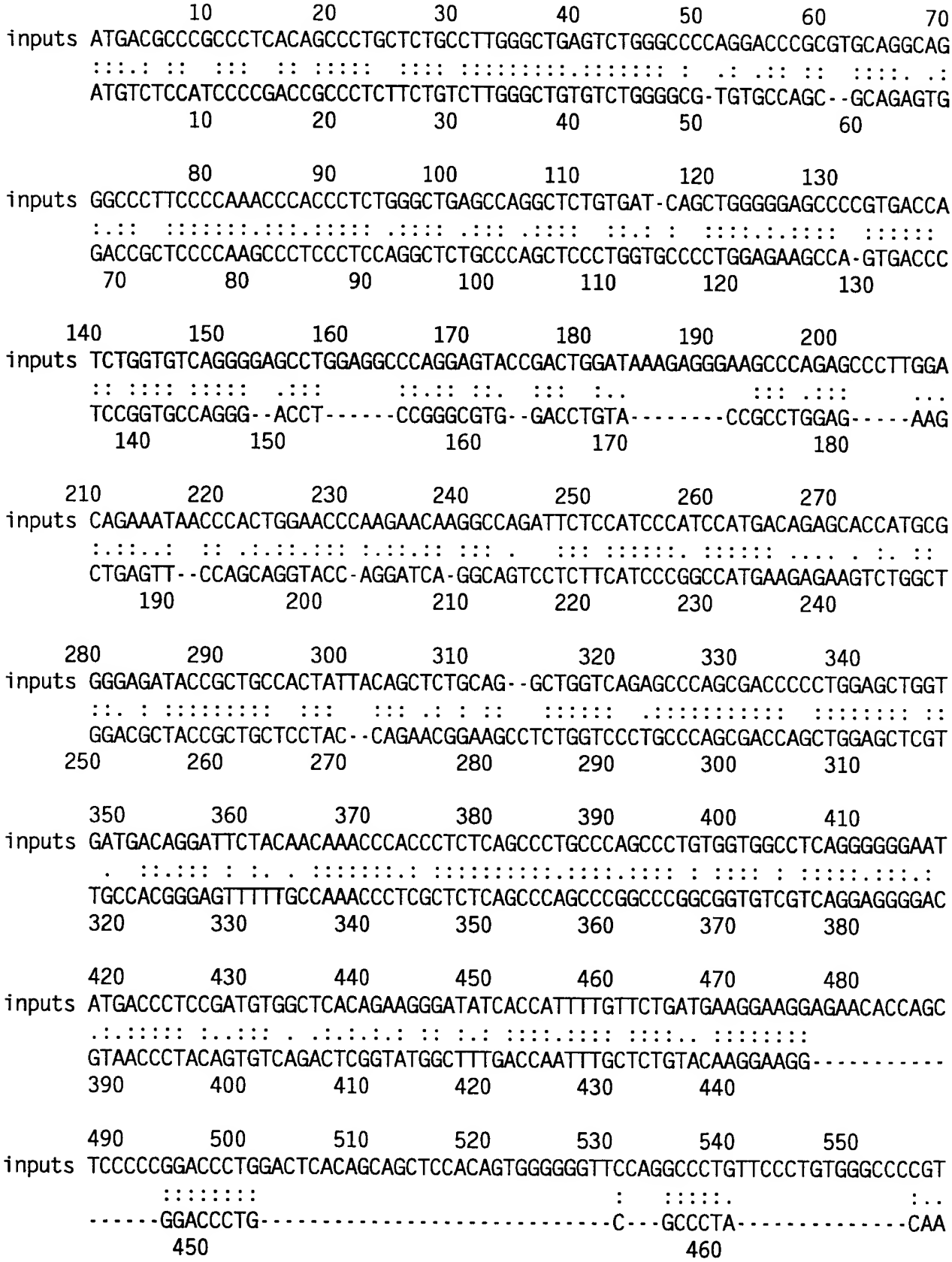


FIG.3A

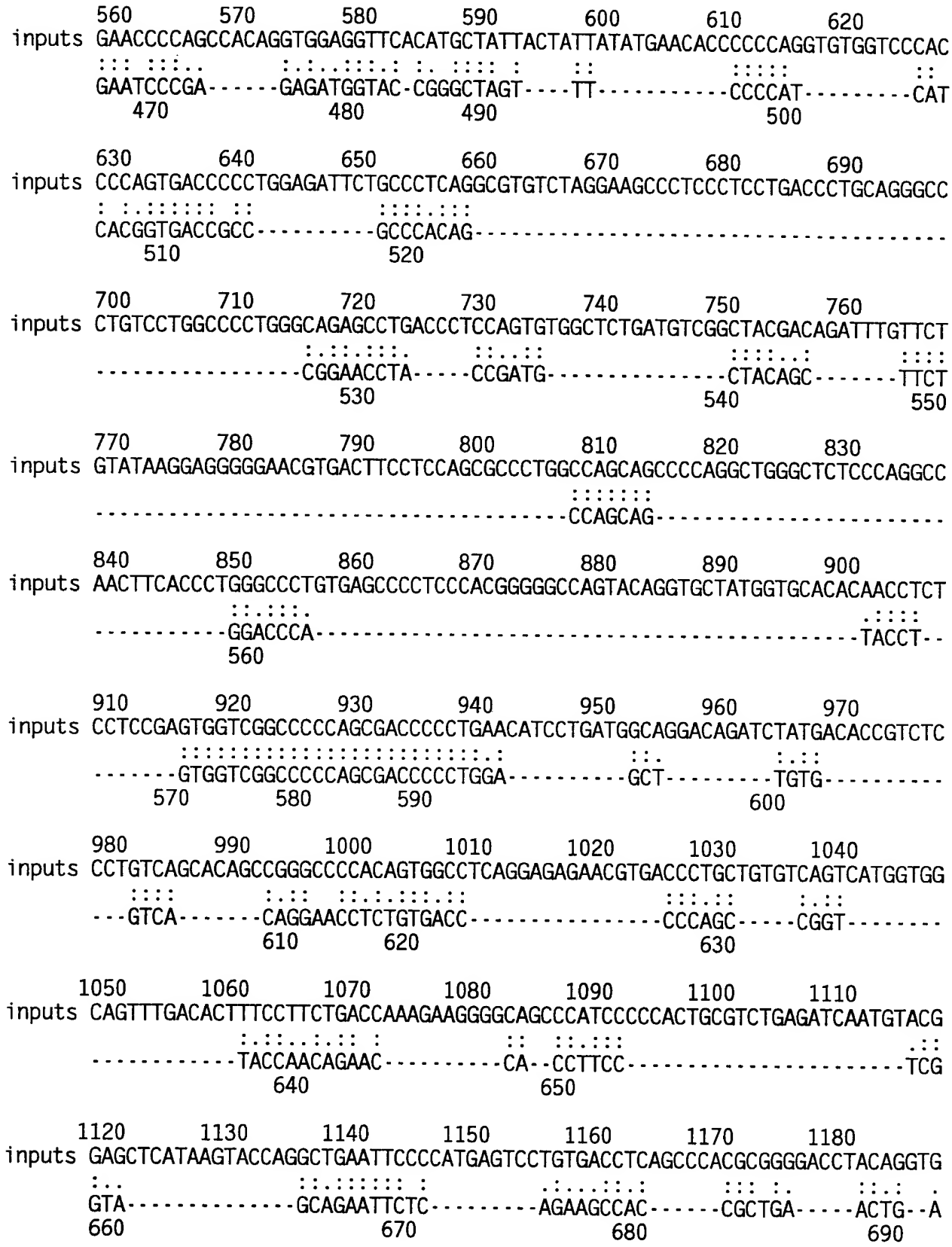

560 570 580 590 600 610 620
inputs GAACCCCAGCCACAGGTGGAGGTTCACATGCTATTACTATTATATGAACACCCCCCAGGTGTGGTCCCAC
GAATCCCGA------GAGATGGTAC-CGGGCTAGT----TT----------CCCCAT---------CAT
470 480 490 500
630 640 650 660 670 680 690
inputs CCCAGTGACCCCCTGGAGATTCTGCCCTCAGGCGTGTCTAGGAAGCCCTCCCTCCTGACCCTGCAGGGCC
CACGGTGACCGCC----------GCCCACAG----------
510 520
700 710 720 730 740 750 760
inputs CTGTCCTGGCCCCTGGGCAGAGCCTGACCCTCCAGTGTGGCTCTGATGTCGGCTACGACAGATTTGTTCT
----------CGGAACCTA-----CCGATG----------CTACAGC-------TTCT
530 540 550
770 780 790 800 810 820 830
inputs GTATAAGGAGGGGGAACGTGACTTCCTCCAGCGCCCTGGCCAGCAGCCCCAGGCTGGGCTCTCCCAGGCC
----------CCAGCAG----------
840 850 860 870 880 890 900
inputs AACTTCACCCTGGGCCCTGTGAGCCCCTCCCACGGGGGCCAGTACAGGTGCTATGGTGCACACAACCTCT
----------GGACCCA----------TACCT--
560
910 920 930 940 950 960 970
inputs CCTCCGAGTGGTCGGCCCCCAGCGACCCCCTGAACATCCTGATGGCAGGACAGATCTATGACACCGTCTC
-------GTGGTCGGCCCCCAGCGACCCCCTGGA----------GCT---------TGTG----------
570 580 590 600
980 990 1000 1010 1020 1030 1040
inputs CCTGTCAGCACAGCCGGGCCCCACAGTGGCCTCAGGAGAGAACGTGACCCTGCTGTGTCAGTCATGGTGG
---GTCA-------CAGGAACCTCTGTGACC----------CCCAGC-----CGGT--------
610 620 630
1050 1060 1070 1080 1090 1100 1110
inputs CAGTTTGACACTTTCCTTCTGACCAAAGAAGGGGCAGCCCATCCCCCACTGCGTCTGAGATCAATGTACG
----------TACCAACAGAAC----------CA--CCTTCC----------TCG
640 650
1120 1130 1140 1150 1160 1170 1180
inputs GAGCTCATAAGTACCAGGCTGAATTCCCCATGAGTCCTGTGACCTCAGCCCACGCGGGGACCTACAGGTG
GTA----------GCAGAATTCTC---------AGAAGCCAC------CGCTGA-----ACTG--A
660 670 680 690

FIG.3B

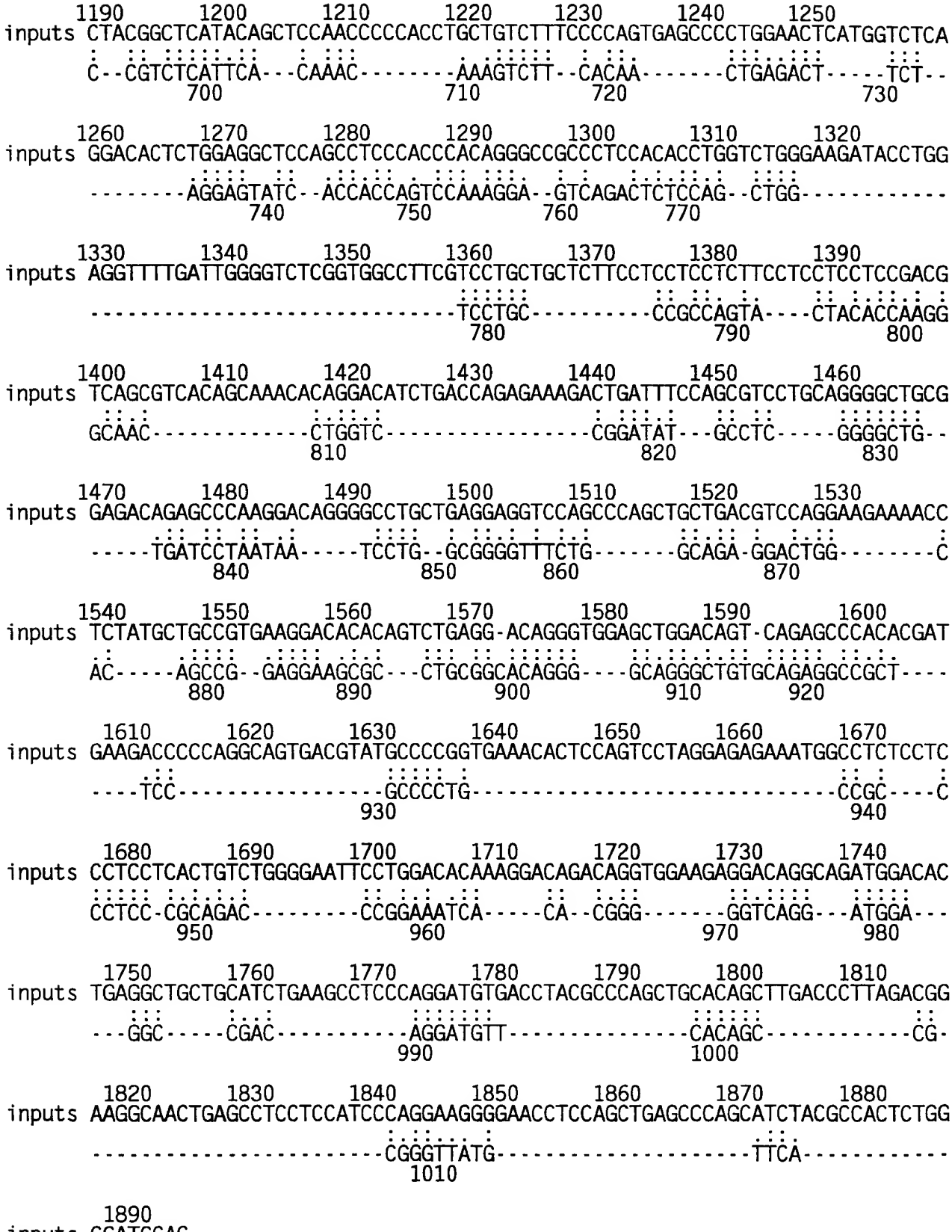

1190 1200 1210 1220 1230 1240 1250
inputs CTACGGCTCATACAGCTCCAACCCCCACCTGCTGTCTTTCCCCAGTGAGCCCCTGGAACTCATGGTCTCA
C--CGTCTCATTCA---CAAAC--------AAAGTCTT--CACAA-------CTGAGACT-----TCT--
700 710 720 730
1260 1270 1280 1290 1300 1310 1320
inputs GGACACTCTGGAGGCTCCAGCCTCCCACCCACAGGGCCGCCCTCCACACCTGGTCTGGGAAGATACCTGG
--------AGGAGTATC--ACCACCAGTCCAAAGGA--GTCAGACTCTCCAG--CTGG-----------
740 750 760 770
1330 1340 1350 1360 1370 1380 1390
inputs AGGTTTTGATTGGGGTCTCGGTGGCCTTCGTCCTGCTGCTCTTCCTCCTCCTCTTCCTCCTCCTCCGACG
----------TCCTGC----------CCGCCAGTA----CTACACCAAGG
780 790 800
1400 1410 1420 1430 1440 1450 1460
inputs TCAGCGTCACAGCAAACACAGGACATCTGACCAGAGAAAGACTGATTTCCAGCGTCCTGCAGGGGCTGCG
GCAAC----------CTGGTC----------CGGATAT---GCCTC-----GGGGCTG--
810 820 830
1470 1480 1490 1500 1510 1520 1530
inputs GAGACAGAGCCCAAGGACAGGGGCCTGCTGAGGAGGTCCAGCCCAGCTGCTGACGTCCAGGAAGAAAACC
-----TGATCCTAATAA-----TCCTG--GCGGGGTTTCTG-------GCAGA-GGACTGG--------C
840 850 860 870
1540 1550 1560 1570 1580 1590 1600
inputs TCTATGCTGCCGTGAAGGACACACAGTCTGAGG-ACAGGGTGGAGCTGGACAGT-CAGAGCCCACACGAT
AC-----AGCCG--GAGGAAGCGC---CTGCGGCACAGGG----GCAGGGCTGTGCAGAGGCCGCT----
880 890 900 910 920
1610 1620 1630 1640 1650 1660 1670
inputs GAAGACCCCCAGGCAGTGACGTATGCCCCGGTGAAACACTCCAGTCCTAGGAGAGAAATGGCCTCTCCTC
----TCC----------GCCCCTG----------CCGC----C
930 940
1680 1690 1700 1710 1720 1730 1740
inputs CCTCCTCACTGTCTGGGGAATTCCTGGACACAAAGGACAGACAGGTGGAAGAGGACAGGCAGATGGACAC
CCTCC-CGCAGAC---------CCGGAAATCA-----CA--CGGG-------GGTCAGG---ATGGA---
950 960 970 980
1750 1760 1770 1780 1790 1800 1810
inputs TGAGGCTGCTGCATCTGAAGCCTCCCAGGATGTGACCTACGCCCAGCTGCACAGCTTGACCCTTAGACGG
---GGC-----CGAC----------AGGATGTT----------CACAGC----------CG-
990 1000
1820 1830 1840 1850 1860 1870 1880
inputs AAGGCAACTGAGCCTCCTCCATCCCAGGAAGGGGAACCTCCAGCTGAGCCCAGCATCTACGCCACTCTGG
----------CGGGTTATG----------TTCA----------
1010
1890
inputs CCATCCAC

FIG.3C

```
                10         20         30         40         50         60
inputs MSPSPTALFCLGLCLG-RVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGPPGVDLYRLEKLSSS----
       :.:. :::.:::: :: :. .:.:::::.: : :.:...   :::.:::.  .. :::.: .:.
       MTPALTALLCLGLSLGPRTRVQAGPFPKPTLWAEPGSVISWGSPVTIWCQGSLEAQEYRLDKEGSPEPLD
                10         20         30         40         50         60         70

                70         80         90        100        110        120        130
inputs RYQ-----DQAVLFIPAMKRSLAGRYRCSYQNGSLWSLPSDQLELVATGVFAKPSLSAQPGPAVSSGGDV
       : .     ..: . :::.    :::::: : ... :: :::.::: :: ..::.::: :.:.:.::::..
       RNNPLEPKNKARFSIPSMTEHHAGRYRCHYYSSAGWSEPSDPLELVMTGFYNKPTLSALPSPVVASGGNM
                80         90        100        110        120        130        140

inputs TLQCQT-----------------------------------------------RY--------------
       ::.: .                                              :.
       TLRCGSQKGYHHFVLMKEGEHQLPRTLDSQQLHSGGFQALFPVGPVNPSHRWRFTCYYYYMNTPQVWSHP
              150        160        170        180        190        200        210

                                                 140        150
inputs -------------------------------------------GFDQFALYKEGDP----------------
                                                   :.:.:::::::.
       SDPLEILPSGVSRKPSLLTLQGPVLAPGQSLTLQCGSDVGYDRFVLYKEGERDFLQRPGQQPQAGLSQAN
              220        230        240        250        260        270        280

                                                                             160
inputs -----------APYK--------------NP-------------------------------ERW--
                 .:.:                .:                                . :
       FTLGPVSPSHGGQYRCYGAHNLSSEWSAPSDPLNILMAGQIYDTVSLSAQPGPTVASGENVTLLCQSWWQ
              290        300        310        320        330        340        350

                                          170        180        190        200
inputs -------------------------YRASFPIITVTAAHSGTYRCYSFSSRDPYLWSAPSDPLELVVTG
                                 :.: :::.  :::.:::::::::.  : .:: : : :::::::.:.:
       FDTFLLTKEGAAHPPLRLRSMYGAHKYQAEFPMSPVTSAHAGTYRCYGSYSSNPHLLSFPSEPLELMVSG
              360        370        380        390        400        410        420

          210        220        230                240        250        260
inputs TSVTPSRLPTEPPSS--VAEFSEATAELTVSFTNKVF--------TTETSRSITTSPKESD--SPAGPA-
        :  .:  :: :::. . . . :.  .:::.  .:           :.  :.... .:   ::::.
       HSGGSSLPPTGPPSTPGLGRYLEVLIGVSVAFVLLLFLLLFLLLRRQRHSKHRTSDQRKTDFQRPAGAAE
              430        440        450        460        470        480        490

             270        280            290                                  .
inputs RQYYTKGNLVRICLGAVIL-----IILAGFLAEDW-------------------.---HSRRKR-------
       .   .: : :  .: .          .  .::.                      :: .:
       TEPKDRGLLRRSSPAADVQEENLYAAVKDTQSEDRVELDSQSPHDEDPQAVTYAPVKHSSPRREMASPPS
              500        510        520        530        540        550        560

             300                          310        320            330
inputs ------LRHRGRAVQ--RPL--------------PPLPPLPQTRK------SHGGQDGGRQDVHSRGLC
              :  ..: :.  :..                ..: .:   ::      :. :.  . .... .
       SLSGEFLDTKDRQVEEDRQMDTEAAASEASQDVTYAQLHSLTLRRKATEPPPSQEGEPPAEPSIYATLAI
              570        580        590        600        610        620        630

inputs S

       H
```

FIG.4

```
            *->GesvtLtCsvsgfgppgvsvtWyfkngk.lgpsllgysysrlesgek
               + vtL+C+        + v  y +  k  ++        r++ +
hT268    41    EKPVTLRCQGP------PGVDLY-RLEKlSSS--------RYQDQ--  70

               anlsegrfsissltLtissvekeDsGtYtCvv<-*
                           ++L i   +++ +G Y+C
hT268    71    ------------AVLFIPAMKRSLAGRYRCSY     90
```

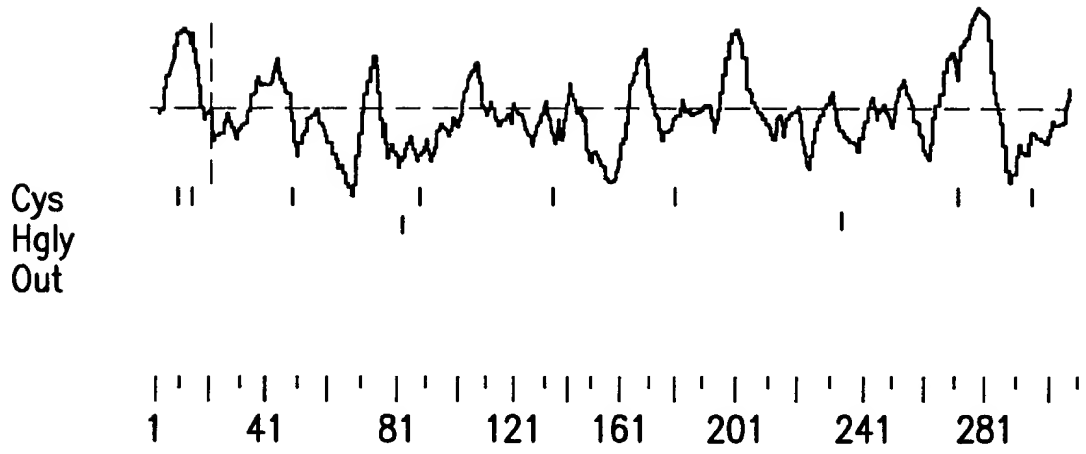
FIG.5A

```
            *->GesvtLtCsvsgfgppgvsvtWyfkngk.lgpsllgysysrlesgek
               G++vtL+C+++    +  ++  y k+g++ +     y+++
hT268   127    GGDVTLQCQTR---YGFDQFALY-KEGDpAP-----YKNPERWYR--  162

               anlsegrfsissltLtissvekeDsGtYtCvv<-*
                          ++++i++v++  sGtY+C
hT268   163    ------------ASFPIITVTAAHSGTYRCYS     182
```

FIG.5B

```
                                                                  M  S  P  A      4
GAGTCGACCCACGCGTCCGCTTCCCTGCTTGGCCACATAGCTCAGGACTGGGTTGCAGAACC ATG TCT CCA GCC    74

 S  P  T  F  F  C  I  G  L  C  V  L  Q  V  I  Q  T  Q  S  G     24
TCA CCC ACT TTC TTC TGT ATT GGG CTG TGT GTA CTG CAA GTG ATC CAA ACA CAG AGT GGC   134

 P  L  P  K  P  S  L  Q  A  Q  P  S  S  L  V  P  L  G  Q  S     44
CCA CTC CCC AAG CCT TCC CTC CAG GCT CAG CCC AGT TCC CTG GTA CCC CTG GGT CAG TCA   194

 V  I  L  R  C  Q  G  P  P  D  V  D  L  Y  R  L  E  K  L  K     64
GTT ATT CTG AGG TGC CAG GGA CCT CCA GAT GTG GAT TTA TAT CGC CTG GAG AAA CTG AAA   254

 P  E  K  Y  E  D  Q  D  F  L  F  I  P  T  M  E  R  S  N  A     84
CCG GAG AAG TAT GAA GAT CAA GAC TTT CTC TTC ATT CCA ACC ATG GAA AGA AGT AAT GCT   314

 G  R  Y  R  C  S  Y  Q  N  G  S  H  W  S  L  P  S  D  Q  L    104
GGA CGG TAT CGA TGC TCT TAT CAG AAT GGG AGT CAC TGG TCT CTC CCA AGT GAC CAG CTT   374

 E  L  I  A  T  G  V  Y  A  K  P  S  L  S  A  H  P  S  S  A    124
GAG CTA ATT GCT ACA GGT GTG TAT GCT AAA CCC TCA CTC TCA GCT CAT CCC AGC TCA GCA   434

 V  P  Q  G  R  D  V  T  L  K  C  Q  S  P  Y  S  F  D  E  F    144
GTC CCT CAA GGC AGG GAT GTG ACT CTG AAG TGC CAG AGC CCA TAC AGT TTT GAT GAA TTC   494

 V  L  Y  K  E  G  D  T  G  P  Y  K  R  P  E  K  W  Y  R  A    164
GTT CTA TAC AAA GAA GGG GAT ACT GGG CCT TAT AAG AGA CCT GAG AAA TGG TAC CGG GCC   554

 N  F  P  I  I  T  V  T  A  A  H  S  G  T  Y  R  C  Y  S  F    184
AAT TTC CCC ATC ATC ACA GTG ACT GCT GCT CAC AGT GGG ACG TAC CGG TGT TAC AGC TTC   614

 S  S  S  S  P  Y  L  W  S  A  P  S  D  P  L  V  L  V  V  T    204
TCC AGC TCA TCT CCA TAC CTG TGG TCA GCC CCG AGT GAC CCT CTA GTG CTT GTG GTT ACT   674

 G  L  S  A  T  P  S  Q  V  P  T  E  E  S  F  P  V  T  E  S    224
GGA CTC TCT GCC ACT CCC AGC CAG GTA CCC ACG GAA GAA TCA TTT CCT GTG ACA GAA TCC   734

 S  R  R  P  S  I  L  P  T  N  K  I  S  T  T  E  K  P  M  N    244
TCC AGG AGA CCT TCC ATC TTA CCC ACA AAC AAA ATA TCT ACA ACT GAA AAG CCT ATG AAT   794

 I  T  A  S  P  E  G  L  S  P  P  I  G  F  A  H  Q  H  Y  A    264
ATC ACT GCC TCT CCA GAG GGG CTG AGC CCT CCA ATT GGT TTT GCT CAT CAG CAC TAT GCC   854

 K  G  N  L  V  R  I  C  L  G  A  T  I  I  I  I  L  L  G  L    284
AAG GGG AAT CTG GTC CGG ATA TGC CTT GGT GCC ACG ATT ATA ATA ATT TTG TTG GGG CTT   914

 L  A  E  D  W  H  S  R  K  K  C  L  Q  H  R  M  R  A  L  Q    304
CTA GCA GAG GAT TGG CAC AGT CGG AAG AAA TGC CTG CAA CAC AGG ATG AGA GCT TTG CAA   974

 R  P  L  P  P  L  P  L  A  *                                   314
AGG CCA CTA CCA CCC CTC CCA CTG GCC TAG                         1004

AAATAACTTGGCTTTCAGCAGAGGGATTGACCAGACATCCATGCACAACCATGGACATCACCACTAGAGCCACAGACAT 1083
GGACATACTCAAGAGTGGGGAGGTTATATAAAAAAATGAGTGTGGAGAATAAATGCAGAGCCAACAAGGTGAAAAAAAA 1162
A                                                                                  1163
```

FIG.6



MSPASPTFFCIGLCVLQVIQTQSGPLPKPSLQAQPSSLVPLGQSVILRCQGPPDVDLYRL
EKLKPEKYEDQDFLFIPTMERSNAGRYRCSYQNGSHWSLPSDQLELIATGVYAKPSLSAH
PSSAVPQGRDVTLKCQSPYSFDEFVLYKEGDTGPYKRPEKWYRANFPIITVTAAHSGTYR
CYSFSSSSPYLWSAPSDPLVLVVTGLSATPSQVPTEESFPVTESSRRPSILPTNKISTTE
KPMNITASPEGLSPPIGFAHQHYAKGNLVRICLGATIIIILLGLLAEDWHSRKKCLQHRM
RALQRPLPPLPLA

FIG.7

```
                10        20        30        40        50        60        70
inputs ATGACGCCCGCCCTCACAGCCCTGCTCTGCCTTGGGCTGAGTCTGGGCCCCAGGACCCGCGTGCAGGCAG
       :::.: :: ::: ::::  ::    .::  :::   ::::..:
       ATGTCTCCAGCC-TCAC--CC----ACTTTCTT---CTGTAT-------------------------
                10               20          30

                80        90       100       110       120       130       140
inputs GGCCCTTCCCCAAACCCACCCTCTGGGCTGAGCCAGGCTCTGTGATCAGCTGGGGGAGCCCCGTGACCAT
                                 :::::::         :::::.:.::
       ----------------------TGGGCTG---------TGTGTACTGC-----------------
                                              40

                150       160       170       180       190       200       210
inputs CTGGTGTCAGGGGAGCCTGGAGGCCCAGGAGTACCGACTGGATAAAGAGGGAAGCCCAGAGCCCTTGGAC
                                 :.:.:..::               ::.: :::::    :::
       ------------------------AAGTGATCC---------------AAACACAGAG----TGG--
                               50                        60             70

                220       230       240       250       260       270       280
inputs AGAAATAACCCACTGGAACCCAAGAACAAGGCCAGATTCTCCATCCCATCCATGACAGAGCACCATGCGG
                 ::::::    :::     ::::          ::.::::: :::: :
       --------CCCACT----CCC-----CAAG---------CCTTCCC-TCCAGG--------------
                         80                        90

                290       300       310       320       330       340       350
inputs GGAGATACCGCTGCCACTATTACAGCTCTGCAGGCTGGTCAGAGCCCAGCGACCCCCTGGAGCTGGTGAT
                 : :.:::                        :::. :::.: :. ::::::::. :.:
       --------CTCAGCC----------------------CAGTTCCCTG-GTACCCCTGGGTCAG-----
                100                             110       120

                360       370       380       390       400       410       420
inputs GACAGGATTCTACAACAAACCCACCCTCTCAGCCCTGCCCAGCCCTGTGGTGGCCTCAGGGGGGAATATG
                .:::  :: :.:                                ::.::::: :  :::::.
       -TCAG--TTATTC-------------------------------TGAGGTG-C--CAGGGA--------
       130                                         140       150

                430       440       450       460       470       480
inputs ACCCTCC-GATGTGGCTCACAGAAGGGATATCACCATTTTGTTCTGATGAAGGAAGGAGAACACCAGCTC
                 ::::: :::::::          :   :::::.::.  . ...:::::..
       --CCTCCAGATGTGG--------ATTTATATCGCCTGGAGAAACTGAAA------------------
            160               170       180       190

     490       500       510       520       530       540       550
inputs CCCCGGACCCTGGACTCACAGCAGCTCCACAGTGGGGGGTTCCAGGCCCTGTTCCCTGTGGGCCCCGTGA
                 :::::     ::                ::::. :..:.:: ::.:    ::: ::         :.:
       --CCGGA-----GA---------------AGTATGAAGATCAAGAC---TTTCTCTT-------CATT-
                                    200       210       220
```

FIG. 8A

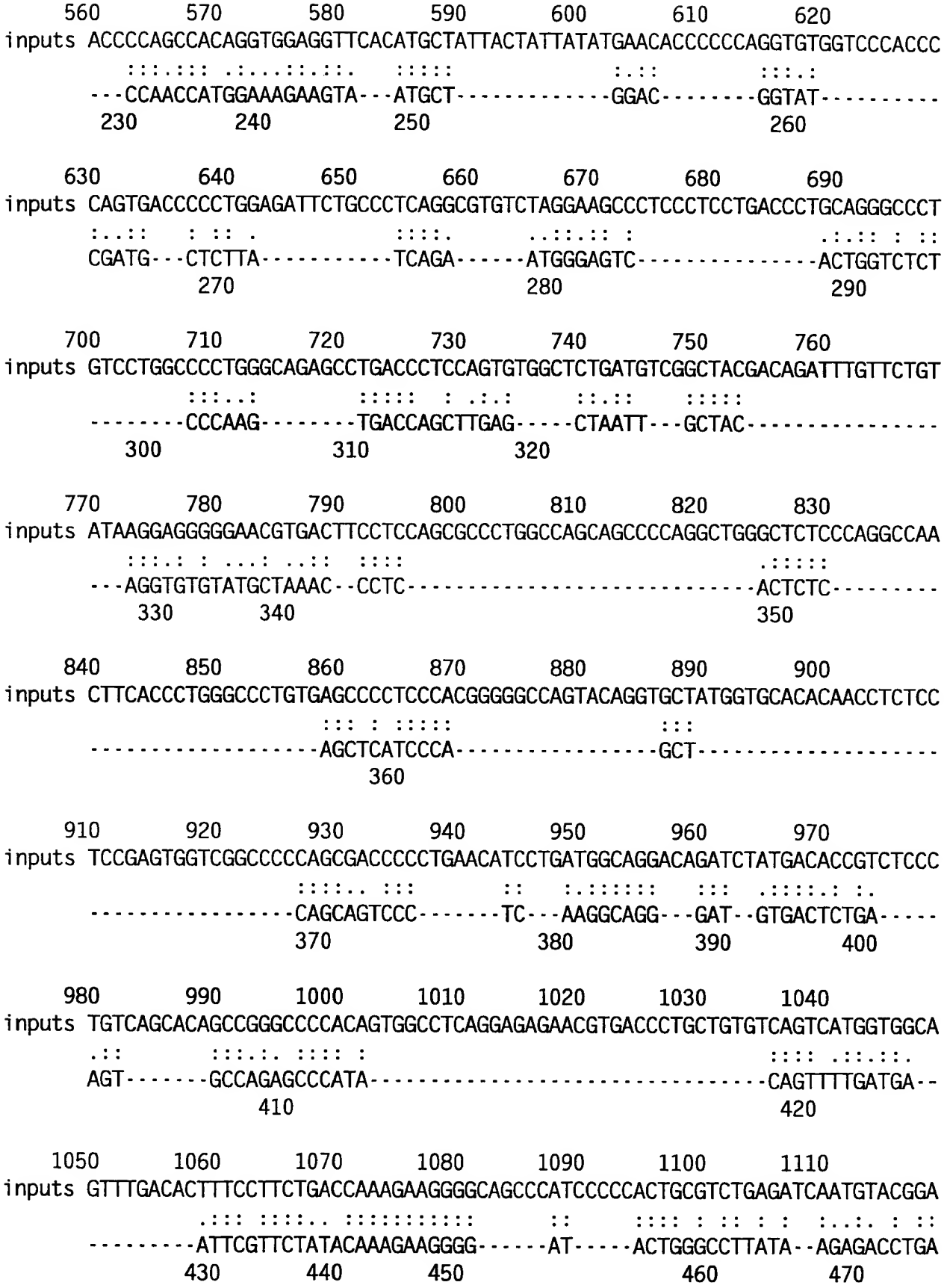

560 570 580 590 600 610 620
inputs ACCCCAGCCACAGGTGGAGGTTCACATGCTATTACTATTATATGAACACCCCCCAGGTGTGGTCCCACCC
---CCAACCATGGAAAGAAGTA---ATGCT----------GGAC--------GGTAT----------
230 240 250 260
630 640 650 660 670 680 690
inputs CAGTGACCCCCTGGAGATTCTGCCCTCAGGCGTGTCTAGGAAGCCCTCCCTCCTGACCCTGCAGGGCCCT
CGATG---CTCTTA----------TCAGA------ATGGGAGTC--------------ACTGGTCTCT
270 280 290
700 710 720 730 740 750 760
inputs GTCCTGGCCCCTGGGCAGAGCCTGACCCTCCAGTGTGGCTCTGATGTCGGCTACGACAGATTTGTTCTGT
--------CCCAAG--------TGACCAGCTTGAG-----CTAATT---GCTAC--------------
300 310 320
770 780 790 800 810 820 830
inputs ATAAGGAGGGGGAACGTGACTTCCTCCAGCGCCCTGGCCAGCAGCCCCAGGCTGGGCTCTCCCAGGCCAA
---AGGTGTGTATGCTAAAC--CCTC----------ACTCTC---------
330 340 350
840 850 860 870 880 890 900
inputs CTTCACCCTGGGCCCTGTGAGCCCCTCCCACGGGGGCCAGTACAGGTGCTATGGTGCACACAACCTCTCC
------------------AGCTCATCCCA----------GCT----------
360
910 920 930 940 950 960 970
inputs TCCGAGTGGTCGGCCCCCAGCGACCCCCTGAACATCCTGATGGCAGGACAGATCTATGACACCGTCTCCC
----------CAGCAGTCCC-------TC---AAGGCAGG---GAT--GTGACTCTGA-----
370 380 390 400
980 990 1000 1010 1020 1030 1040
inputs TGTCAGCACAGCCGGGCCCCACAGTGGCCTCAGGAGAGAACGTGACCCTGCTGTGTCAGTCATGGTGGCA
AGT-------GCCAGAGCCCATA----------CAGTTTTGATGA--
410 420
1050 1060 1070 1080 1090 1100 1110
inputs GTTTGACACTTTCCTTCTGACCAAAGAAGGGGCAGCCCATCCCCCACTGCGTCTGAGATCAATGTACGGA
---------ATTCGTTCTATACAAAGAAGGGG------AT-----ACTGGGCCTTATA--AGAGACCTGA
430 440 450 460 470

FIG.8B

```
    1120       1130       1140       1150       1160       1170       1180
inputs GCTCATAAGTACCAGGCTGAATTCCCCATGAGTCCTGTGACCTCAGCCCACGCGGGGACCTACAGGTGCT
       :   :...:::::.::: .:.:::::::::  :   :.:::::  :.:: :::.  ::::: ::: :::: :
       G--AAATGGTACCGGGCCAATTTCCCCATCATCACAGTGACTGCTGCTCACAGTGGGACGTACCGGTGTT
          480        490        500        510        520        530        540

    1190       1200       1210       1220       1230       1240       1250
inputs ACGGCTCATACAGCTCCAACCCCCACCTGCTGTCTTTCCCCAGTGAGCCCCTGGAACTCATGGTCTCAGG
       ::.:::  : ::::::  .  ::  :::::  :::.  ::: ::::: :: ::.:..:: .:::: .:.::
       ACAGCTTCTCCAGCTCATCTCCATACCTGTGGTCAGCCCCGAGTGACCCTCTAGTGCTTGTGGTTACTGG
          550        560        570        580        590        600        610

    1260       1270       1280       1290       1300       1310       1320
inputs ACACTCTGGAGGCTCCAGCCTCCCACCCACAGGGCCGCCCTCCACACCTGGTCTGGGAAGATACCTGGAG
       ::.::::::      :::  :::::: ::  :::   .::::.        ::. .:... ..:.::::
       ACTCTCTG------CCA--CTCCCAGCC--AGGT--ACCCAC-------GGA-AGAATCATTTCCTG---
          620                630           640                650        660

    1330       1340       1350       1360       1370       1380       1390
inputs GTTTTGATTGGGGTCTCGGTGGCCTTCGTCCTGCTGCTCTTCCTCCTCCTCTTCCTCCTCCTCCGACGTC
          :::          :.:.. :::    ::.: .:  :::::.      :::: :    ::.: .::..
       ----TGA---------CAGAATCCT----CCAGGAGACCTTCCA-----TCTTAC----CCACAAACAAA
                  670           680            690           700

    1400       1410       1420       1430       1440       1450       1460
inputs AGCGTCACAGCAAACACAGGACATCTGACCAGAGAAAGACTGATTTCCAGCGTCCTGCAGGGGCTGCGGA
       :   : .:.:.:::   :.:.:    ...::..:::...:  : : ::. : ::::: ::::::::
       A---TATCTACAA---CTGAA----AAGCCTATGAATATC--ACTGCCT-C-TCCAG-AGGGGCTG----
     710          720           730          740          750

    1470       1480       1490       1500       1510       1520       1530
inputs GACAGAGCCCAAGGACAGGGGCCTGCTGAGGAGGTCCAGCCCAGCTGCTGACGTCCAGGAAGAAAACCTC
          :::::.          ::     :. .:::  .:: :: :.:::.                    :
       -----AGCCCT----------CC-----AATTGGTTTTGCTCATCAGCA------------------C
            760                      770       780

    1540       1550       1560       1570       1580       1590       1600
inputs TATGCTGCCGTGAAGGACACACAGTCTGAGGACAGGGTGGAGCTGGACAGTCAGAGCCCACACGATGAAG
       :::::                              ::.:: :.: ::::.:              ::.. :.:
       TATGC--------------------------CAAGGGGAATCTGGTC-------------CGGATATG
        790                                  800                      810

    1610       1620       1630       1640       1650       1660       1670
inputs ACCCCCAGGCAGTGACGTATGCCCCGGTGAAACACTCCAGTCCTAGGAGAGAAATGGCCTCTCCTCCCTC
          :: .::          :::: ::.:              :: .: :....::
       ---CCTTGG----------TGCCACGAT--------------TATAATAATTTTGT------------
            820                830                      840

    1680       1690       1700       1710       1720       1730       1740
inputs CTCACTGTCTGGGGAATTCCTGGACACAAAGGACAGACAGGTGGAAGAGGACAGGCAGATGGACACTGAG
                :::::.:  ::.:  ::.::::.::.:           :::: :.::.:.:      :
       ---------TGGGGCTT--CTAG---CAGAGGATTGGC-----------ACAGTCGGAAGAA-----AT
                   850           860                  870        880
```

FIG.8C

```
    1750       1760       1770       1780       1790       1800       1810
inputs GCTGCTGCATCTGAAGCCTCCCAGGATGTGACCTACGCCCAGCTGCACAGCTTGACCCTTAGACGGAAGG
       ::  ::::::.:.          ::::::::.::                   :::: .:          .::::
       GC--CTGCAACA---------CAGGATGAGA-----------------GCTTTGC---------AAAGG
             890                 900                         910

    1820       1830       1840       1850       1860       1870       1880
inputs CAACTGAGCCTCCTCCATCCCAGGAAGGGGAACCTCCAGCTGAGCCCAGCATCTACGCCACTCTGGCCAT
       : :::.     ::.::                 :::::                          :.:::::::
       CCACTA-----CCACC---------------CCTCC----------------------CACTGGCC--
         920                           930

    1890
inputs CCAC
```

FIG. 8D

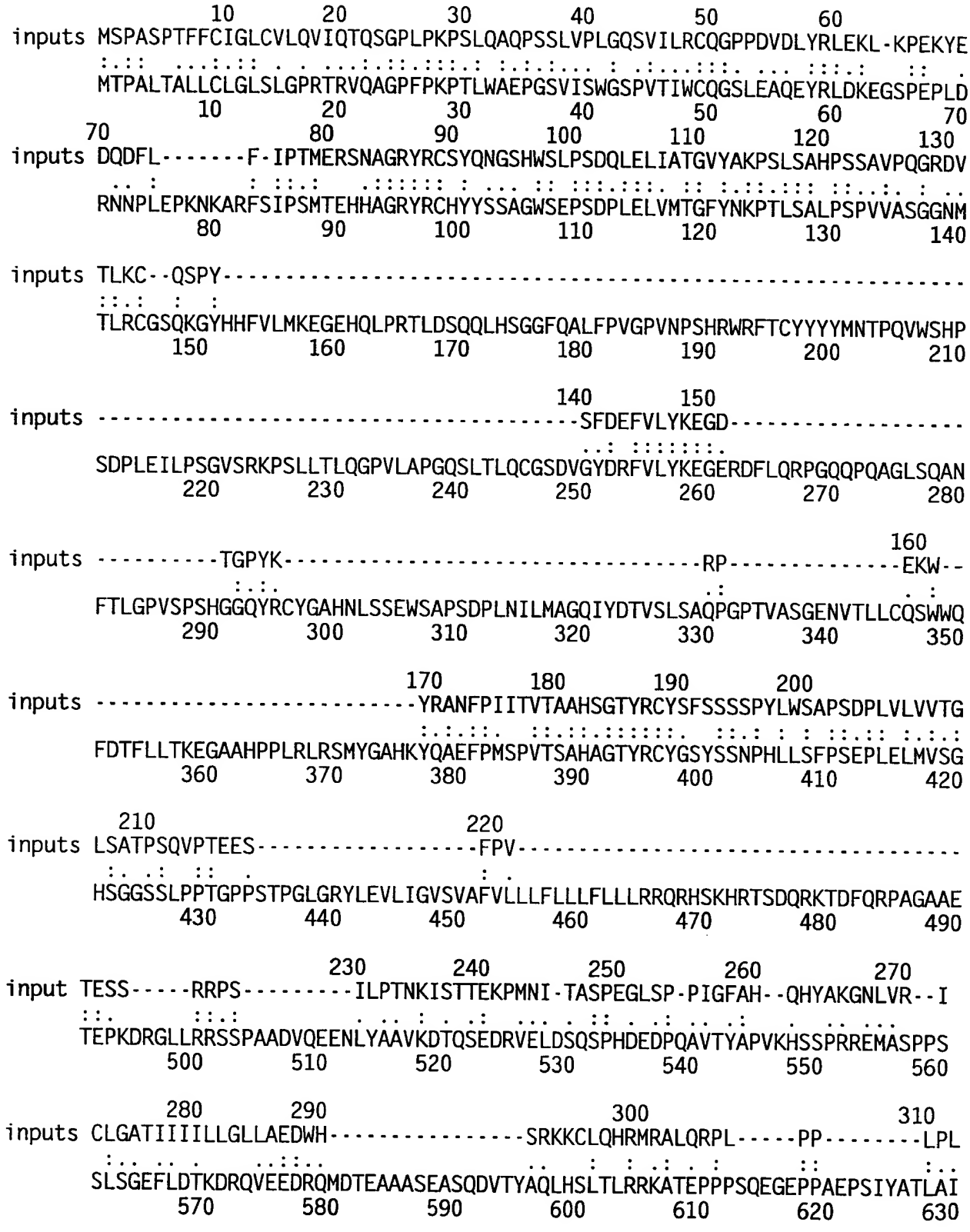


FIG. 9

```
                *->GesvtLtCsvsgfgppgvsvtWyfkngk.lgpsllgysysrlesgek
                   G+sv L+C+        ++v  y +  k ++        +++e +
mT268     42       GQSVILRCQGP------PDVDLY-RLEKlKP--------EKYEDQ-- 71

                   anlsegrfsissltLtissvekeDsGtYtCvv<-*
                                L i + e++++G Y+C
mT268     72       -----------DFLFIPTMERSNAGRYRCSY     91
```

FIG.10A

```
                *->GesvtLtCsvsgfgppgvsvtWyfkngk.lgpsllgysysrlesgek
                   G +vtL C++        ++  y k+g++ +       Y+r+e   +
mT268     128      GRDVTLKCQSP---YSFDEFVLY-KEGDtGP-------YKRPEKW-Y 162

                   anlsegrfsissltLtissvekeDsGtYtCvv<-*
                   +             ++i++v++  sGtY+C
mT268     163      RA----------NFPIITVTAAHSGTYRCYS     183
```

FIG.10B

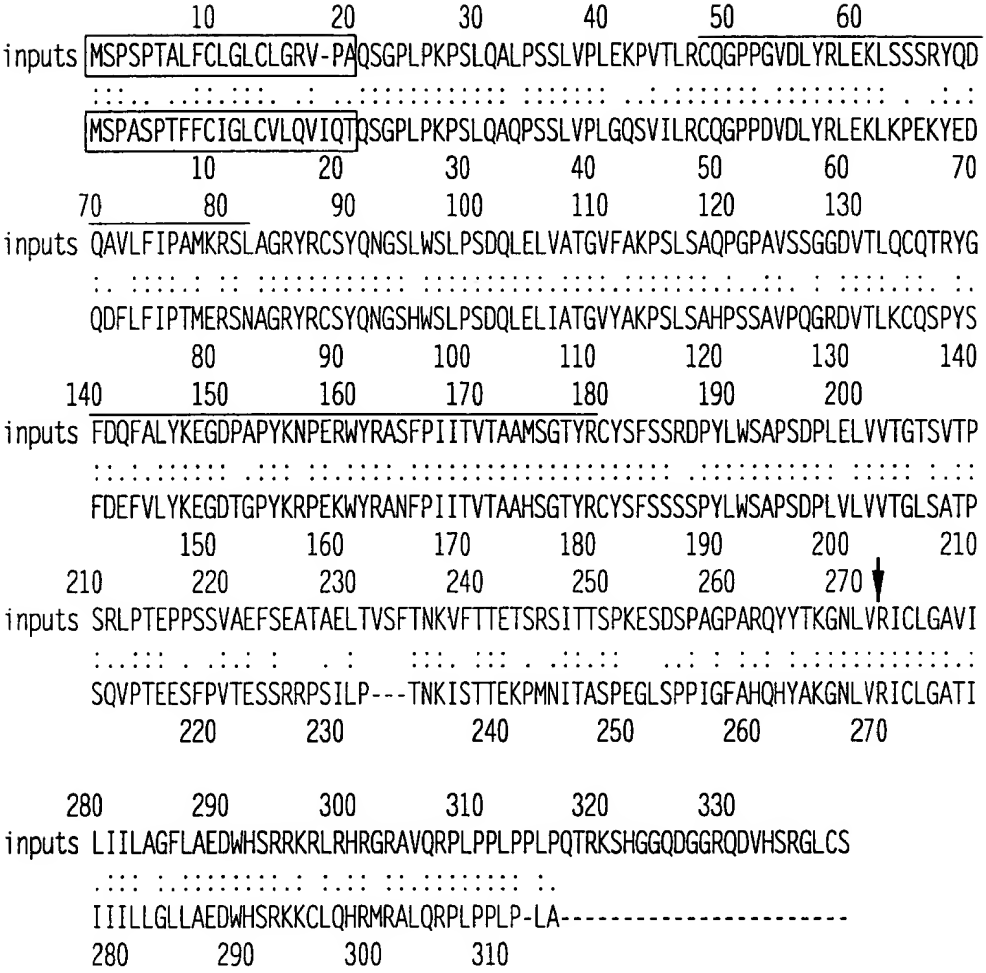

10 20 30 40 50 60
inputs MSPSPTALFCLGLCLGRV-PAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGPPGVDLYRLEKLSSSRYQD
MSPASPTFFCIGLCVLQVIQTQSGPLPKPSLQAQPSSLVPLGQSVILRCQGPPDVDLYRLEKLKPEKYED
10 20 30 40 50 60 70
70 80 90 100 110 120 130
inputs QAVLFIPAMKRSLAGRYRCSYQNGSLWSLPSDQLELVATGVFAKPSLSAQPGPAVSSGGDVTLQCQTRYG
QDFLFIPTMERSNAGRYRCSYQNGSHWSLPSDQLELIATGVYAKPSLSAHPSSAVPQGRDVTLKCQSPYS
80 90 100 110 120 130 140
140 150 160 170 180 190 200
inputs FDQFALYKEGDPAPYKNPERWYRASFPIITVTAAMSGTYRCYSFSSRDPYLWSAPSDPLELVVTGTSVTP
FDEFVLYKEGDTGPYKRPEKWYRANFPIITVTAAHSGTYRCYSFSSSSPYLWSAPSDPLVLVVTGLSATP
150 160 170 180 190 200 210
210 220 230 240 250 260 270
inputs SRLPTEPPSSVAEFSEATAELTVSFTNKVFTTETSRSITTSPKESDSPAGPARQYYTKGNLVRICLGAVI
SQVPTEESFPVTESSRRPSILP---TNKISTTEKPMNITASPEGLSPPIGFAHQHYAKGNLVRICLGATI
220 230 240 250 260 270
280 290 300 310 320 330
inputs LIILAGFLAEDWHSRRKRLRHRGRAVQRPLPPLPPLPQTRKSHGGQDGGRQDVHSRGLCS
IIILLGLLAEDWHSRKKCLQHRMRALQRPLPPLP-LA----------
280 290 300 310

FIG.11

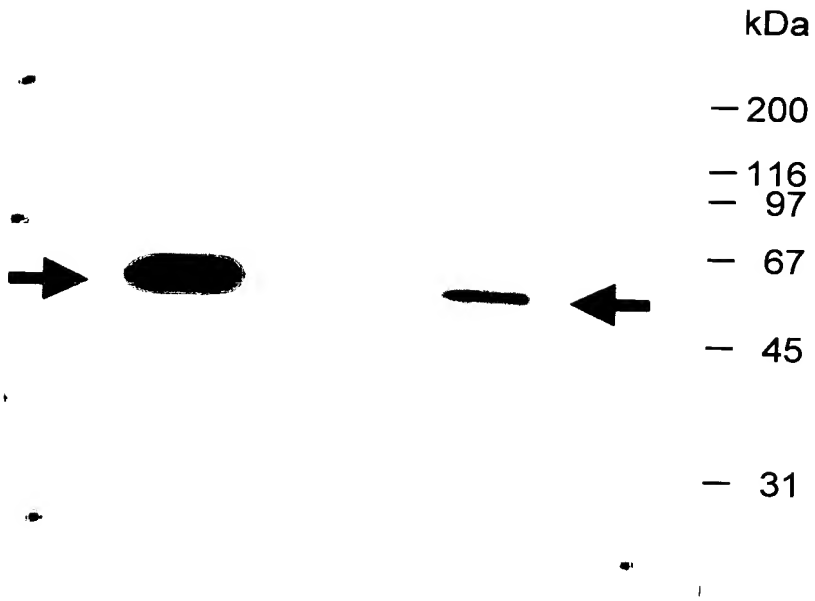


FIG. 12

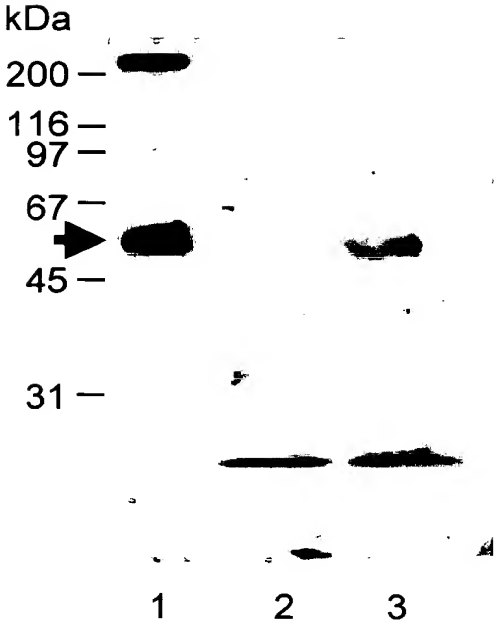


FIG.13A

FIG.13B

FIG.14A

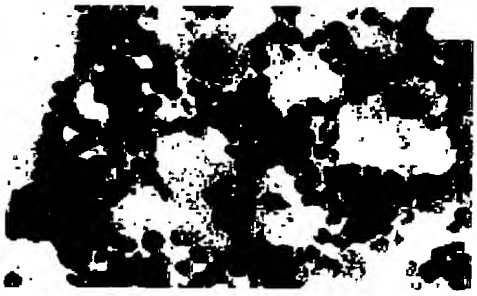


FIG.14B

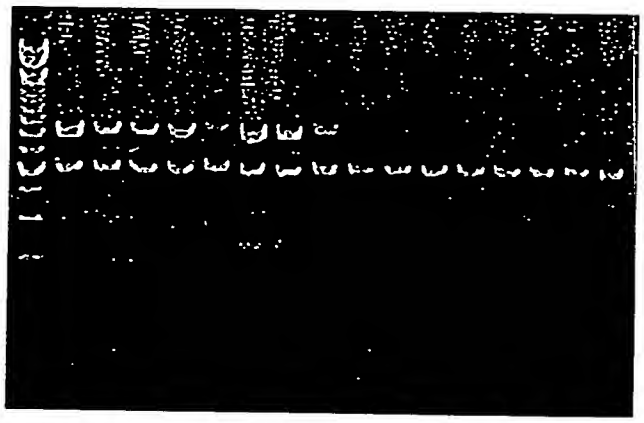


FIG.14C

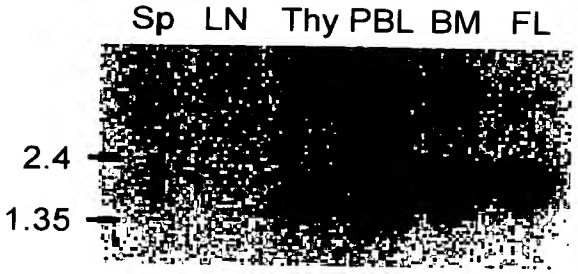


FIG.14D

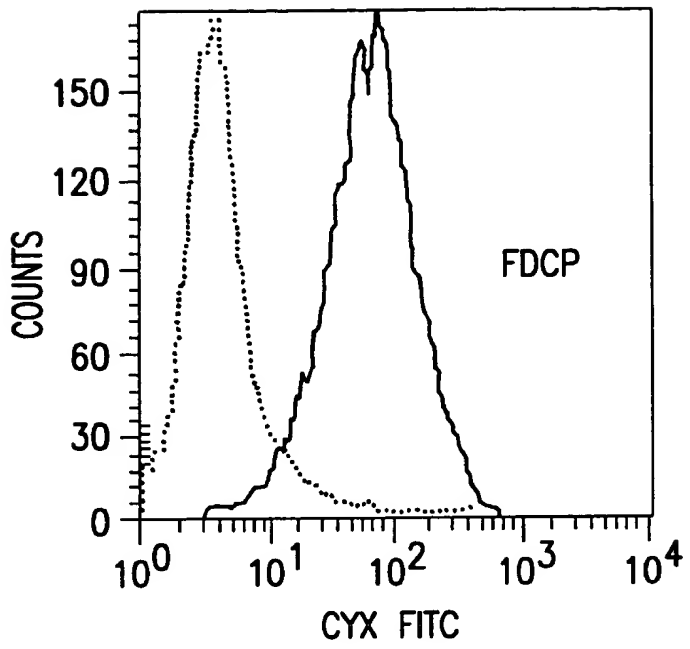


FIG.15A

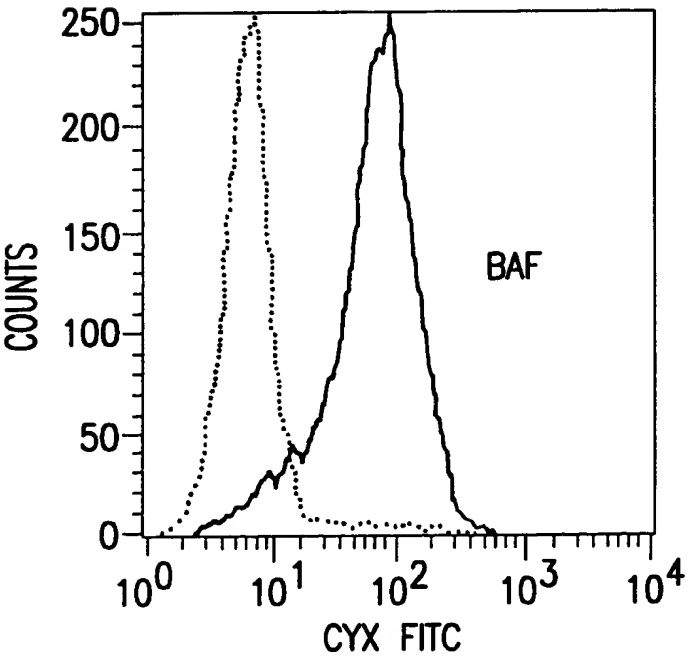


FIG.15B

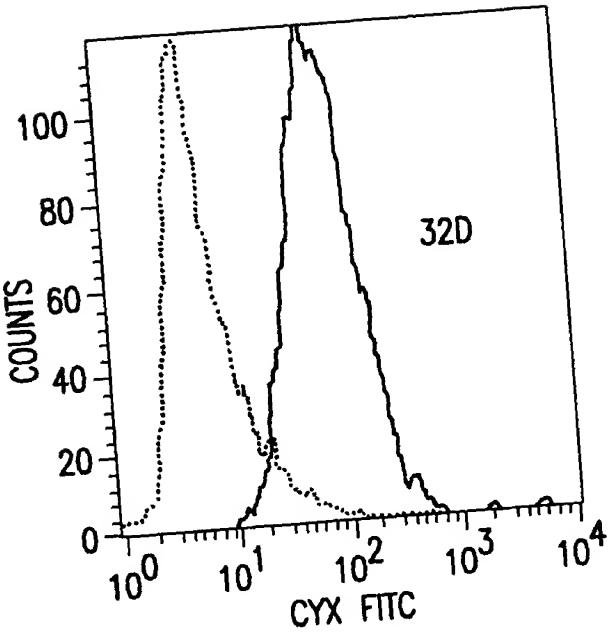


FIG.15C

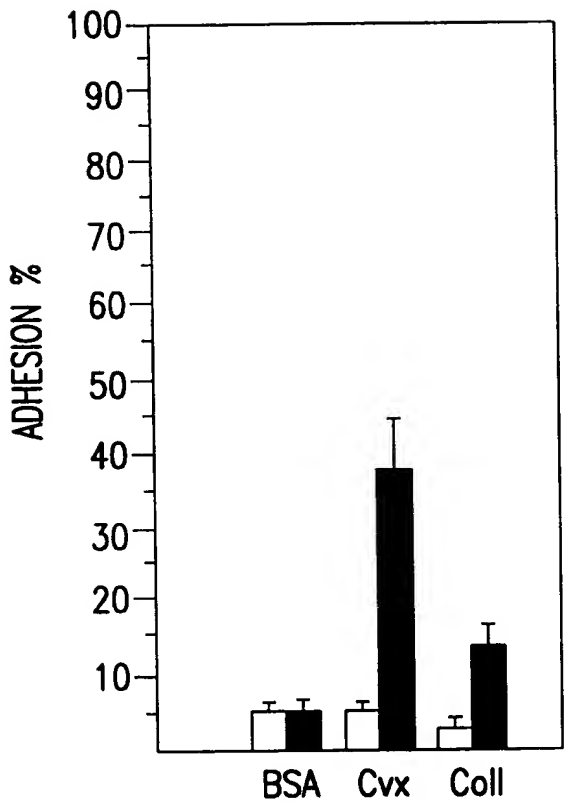


FIG.16A

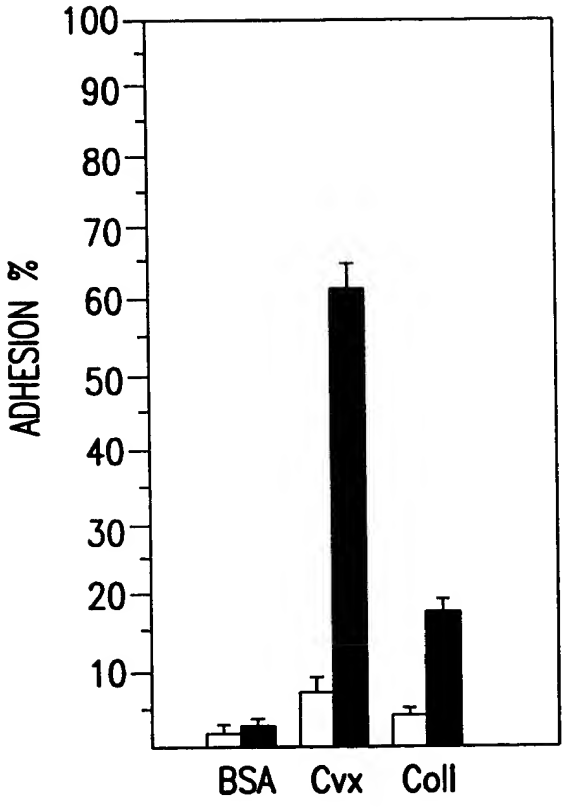


FIG.16B

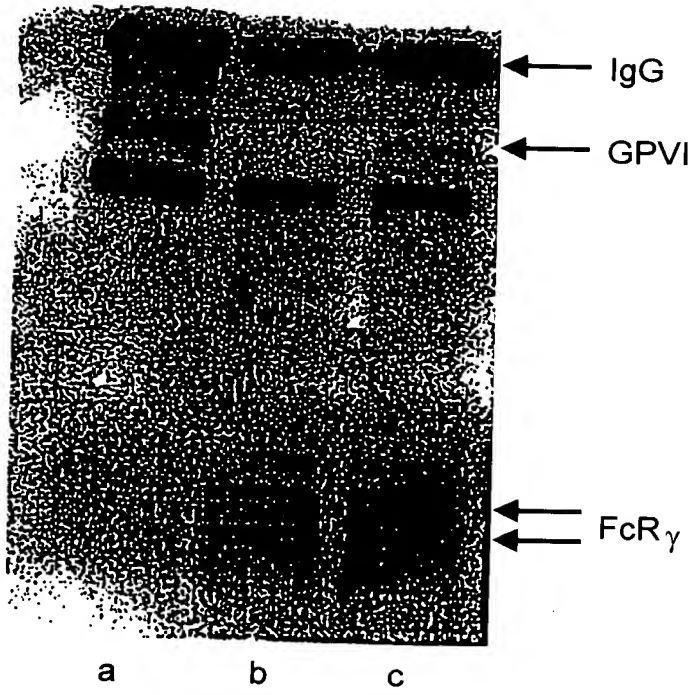


FIG. 17

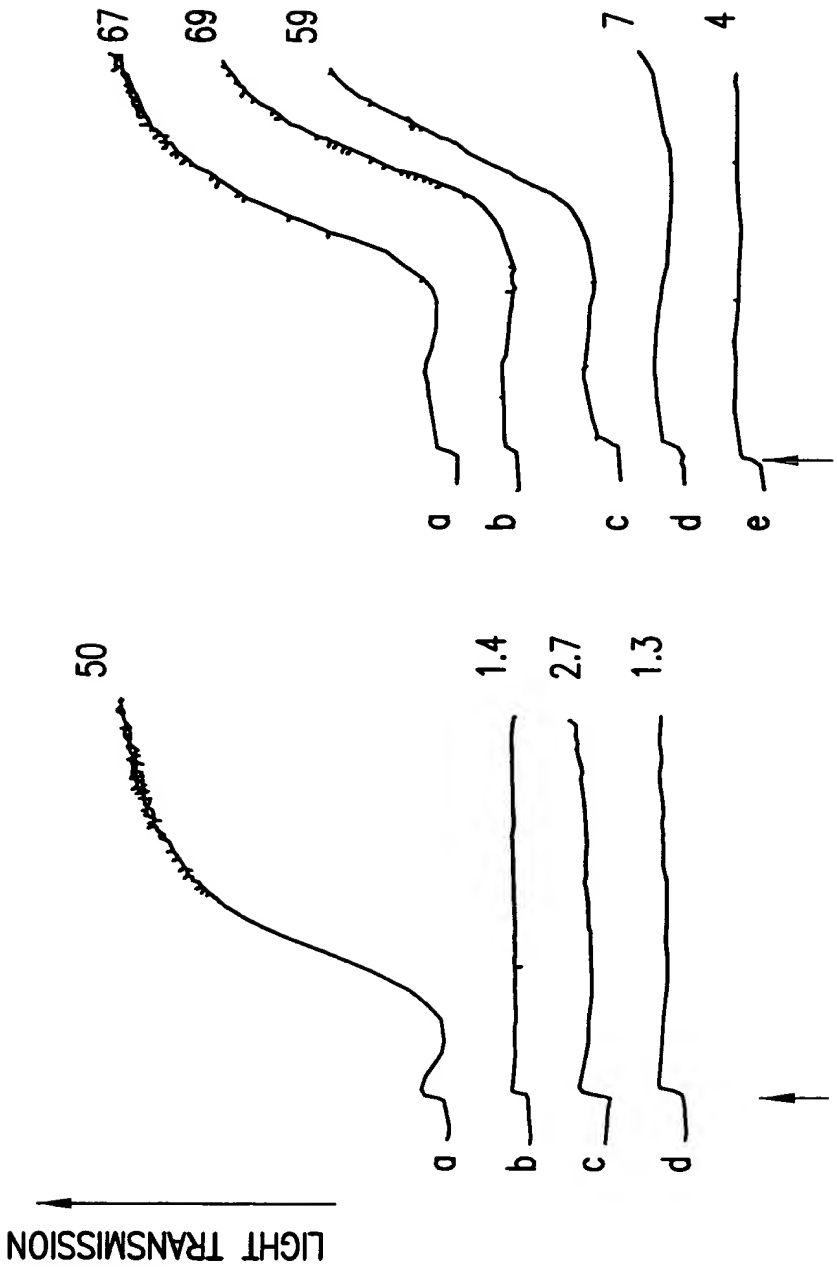


FIG.18A

FIG.18B

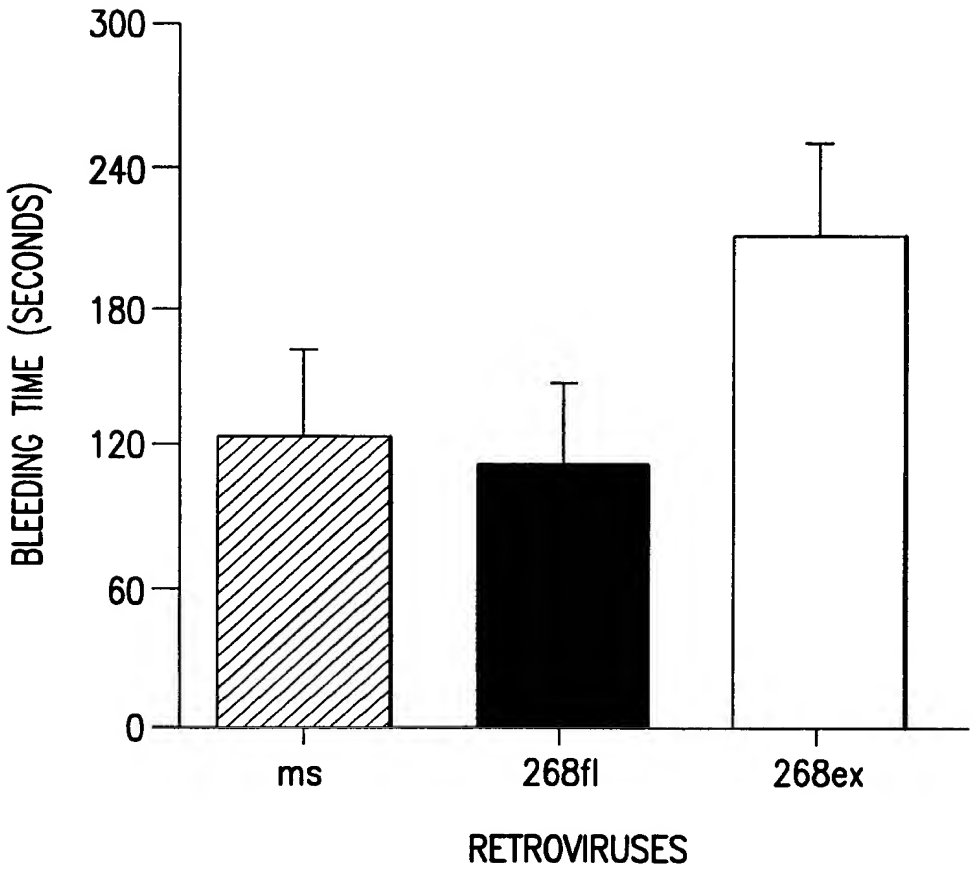

300
240
180
120
60
0
BLEEDING TIME (SECONDS)
ms
268fl
268ex
RETROVIRUSES

FIG.19

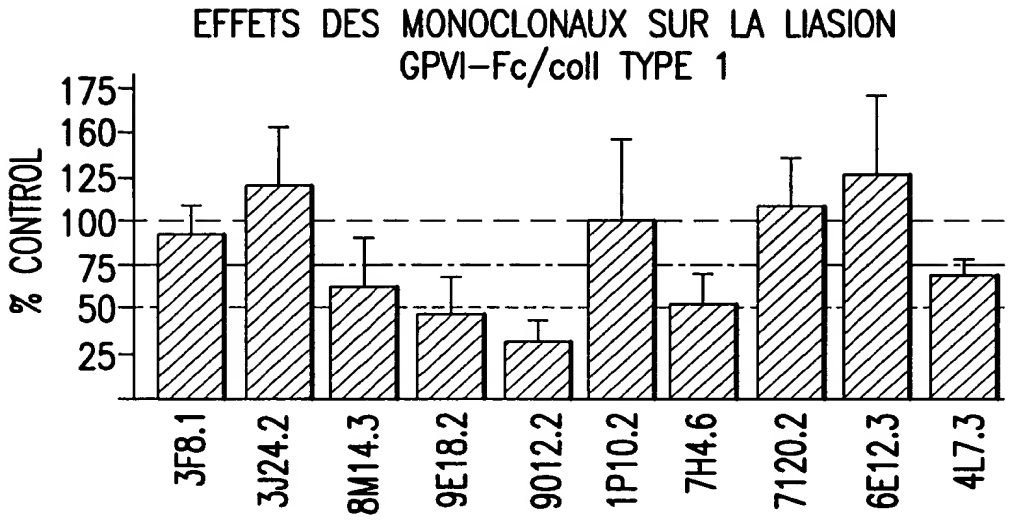

EFFETS DES MONOCLONAUX SUR LA LIASION
GPVI-Fc/coll TYPE 1
% CONTROL
175
160
125
100
75
50
25
3F8.1
3J24.2
8M14.3
9E18.2
9012.2
1P10.2
7H4.6
7120.2
6E12.3
4L7.3

FIG.20

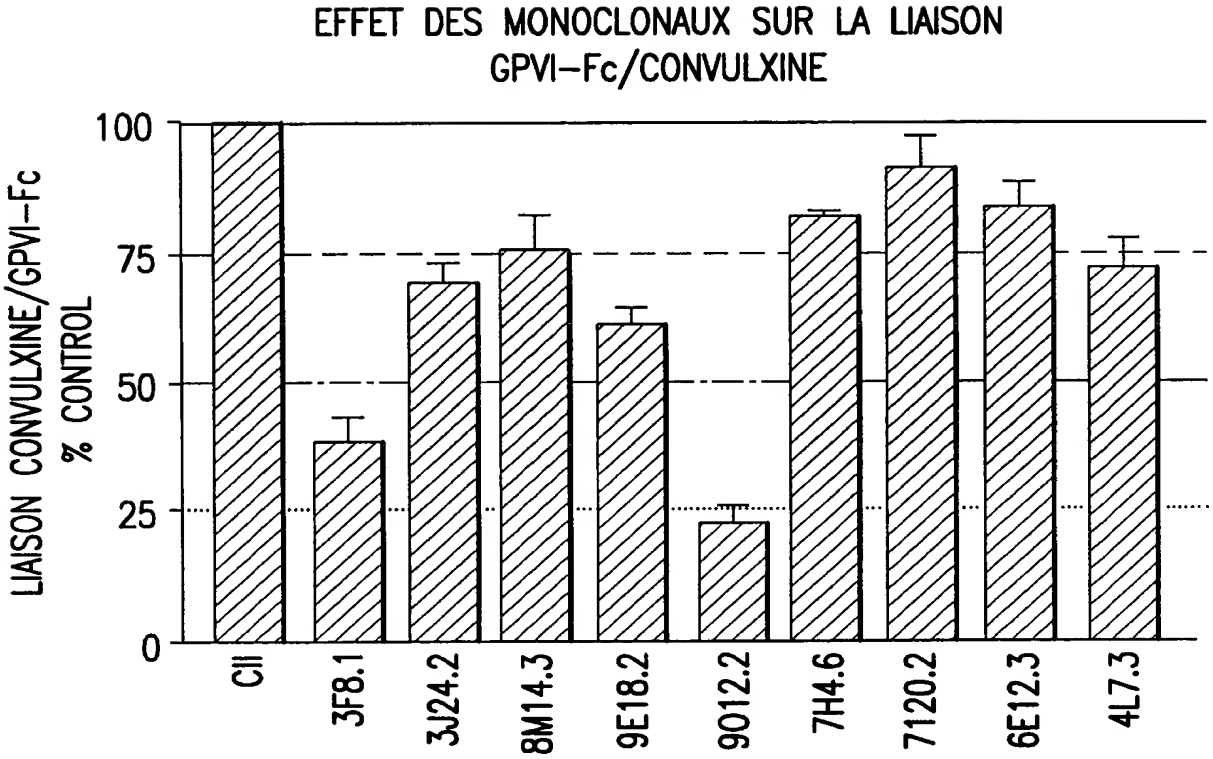

EFFET DES MONOCLONAUX SUR LA LIAISON
GPVI-Fc/CONVULXINE
LIAISON CONVULXINE/GPVI-Fc
% CONTROL
100
75
50
25
0
CII
3F8.1
3J24.2
8M14.3
9E18.2
9012.2
7H4.6
7120.2
6E12.3
4L7.3

FIG.21

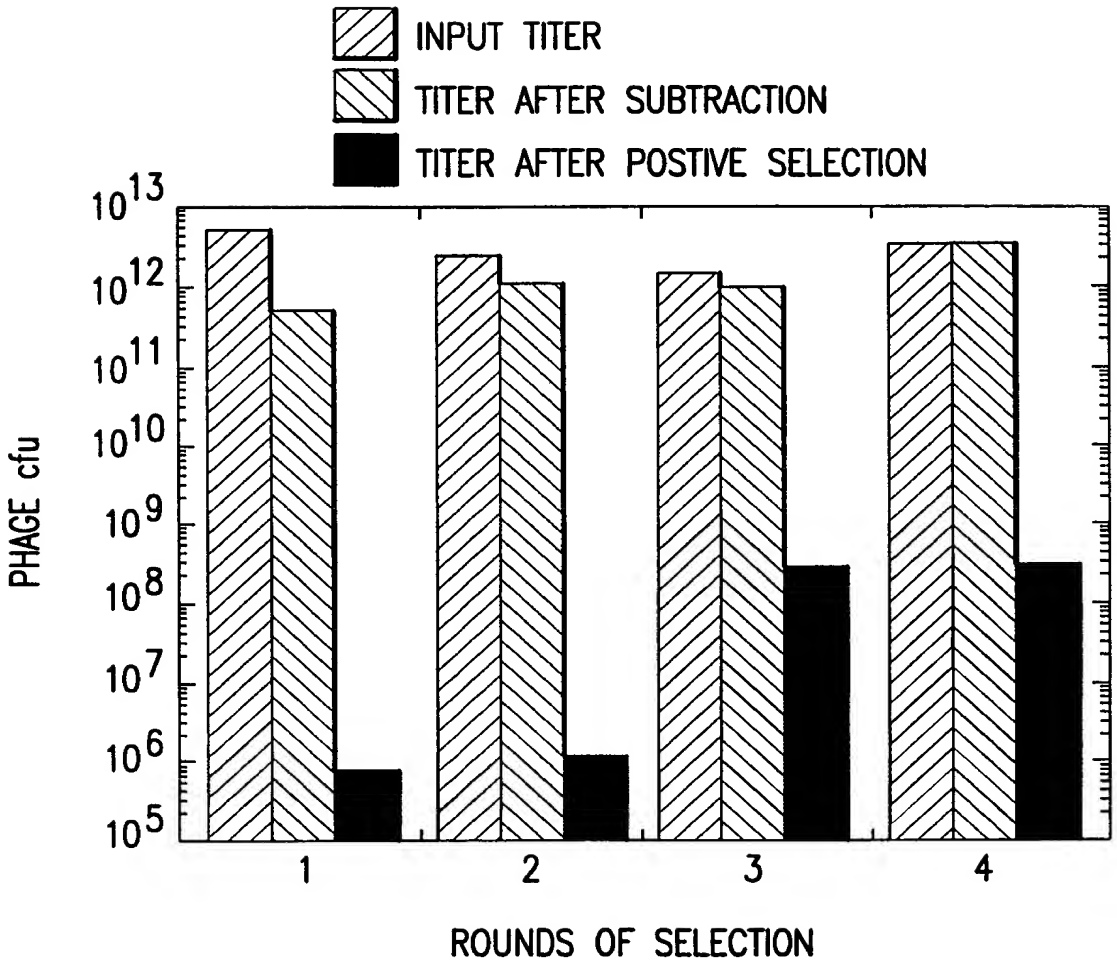

INPUT TITER
TITER AFTER SUBTRACTION
TITER AFTER POSTIVE SELECTION
PHAGE cfu
10^{13}
10^{12}
10^{11}
10^{10}
10^{9}
10^{8}
10^{7}
10^{6}
10^{5}
1
2
3
4
ROUNDS OF SELECTION

FIG.22

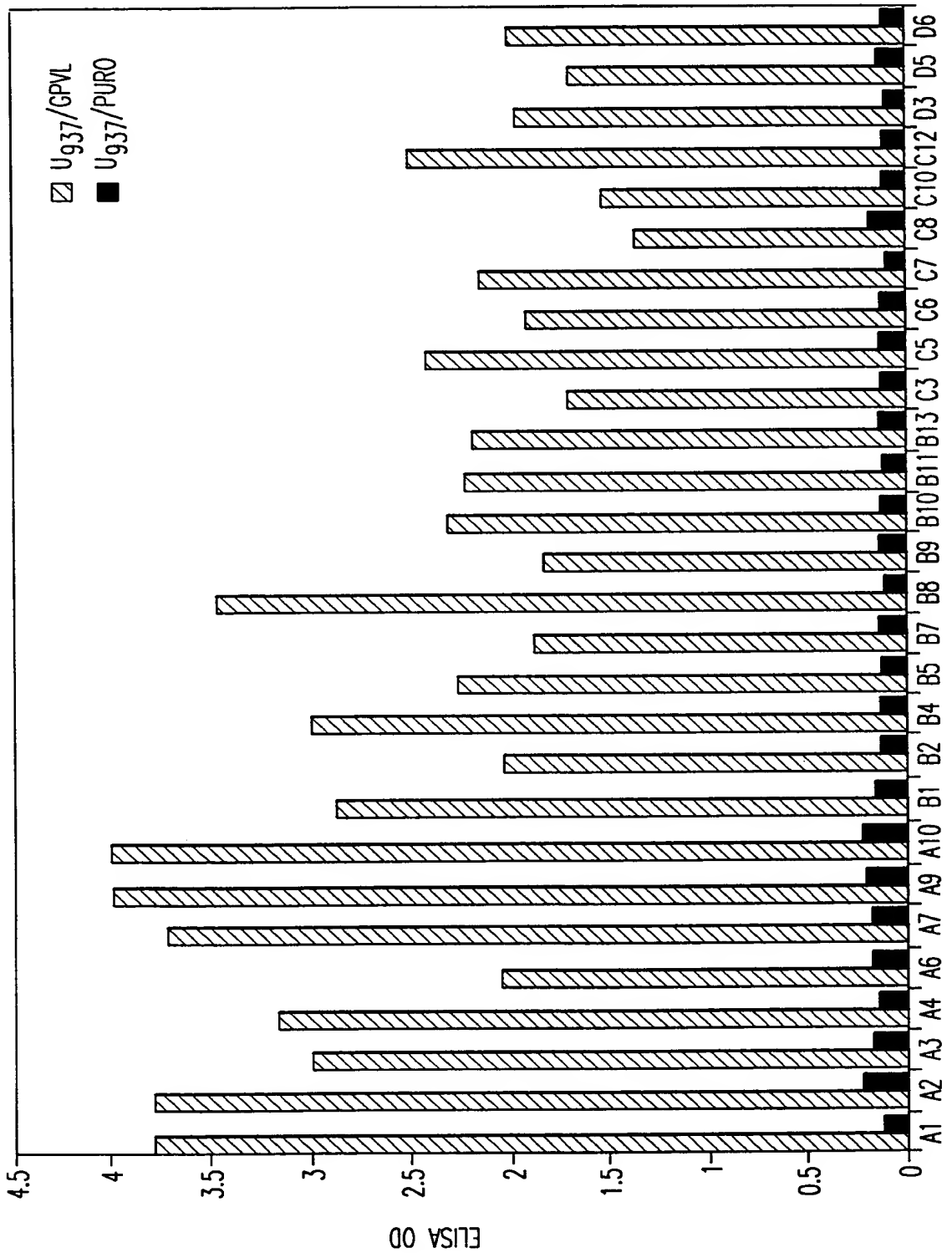

U937/GPVL
U937/PURO
ELISA OD
4.5
4
3.5
3
2.5
2
1.5
1
0.5
0
A1
A2
A3
A4
A6
A7
A9
A10
B1
B2
B4
B5
B7
B8
B9
B10
B11
B13
C3
C5
C6
C7
C8
C10
C12
D3
D5
D6
CLONE 10

FIG.23A

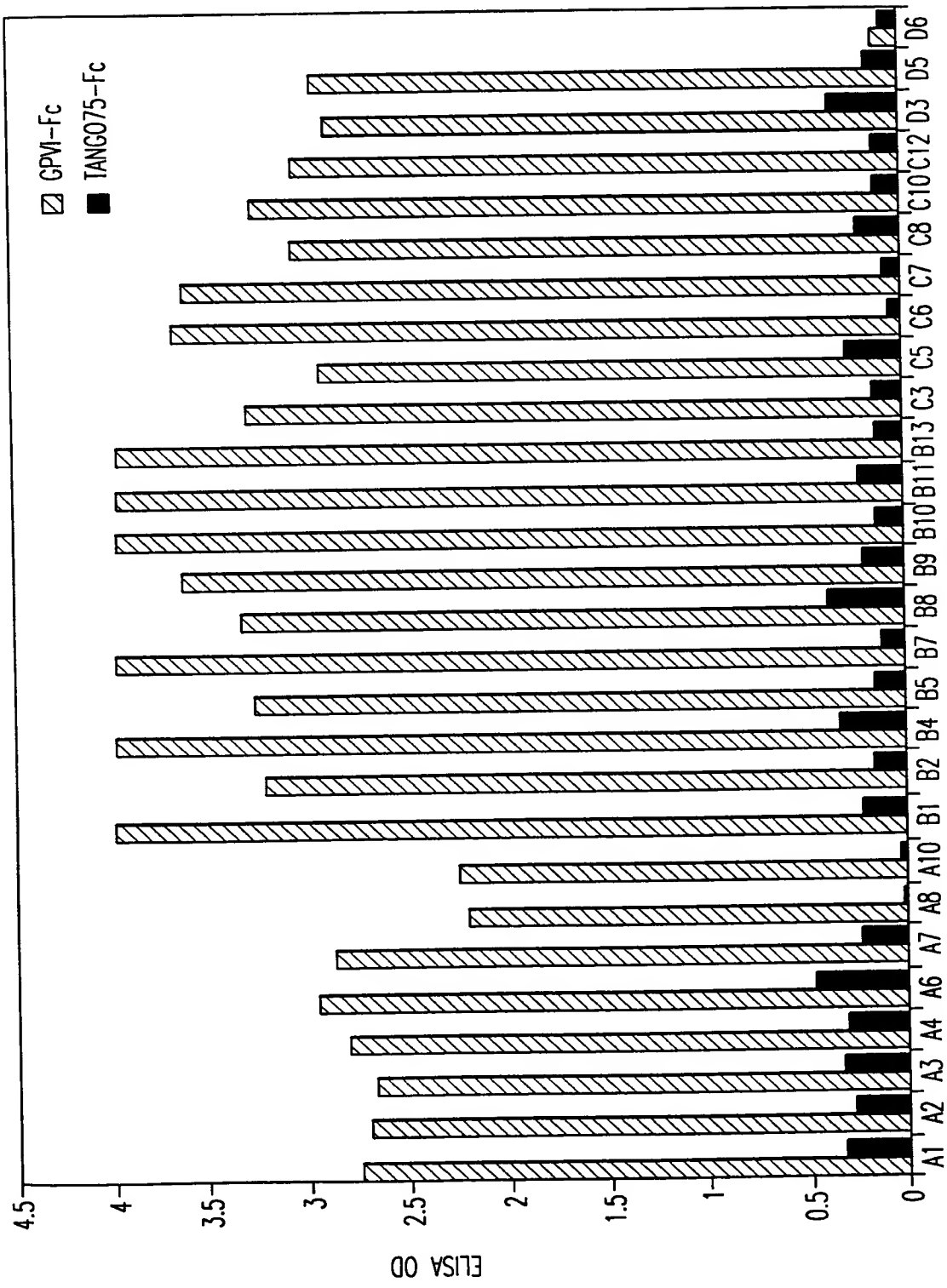

GPVI-Fc
TANGO75-Fc
ELISA OD
4.5
4
3.5
3
2.5
2
1.5
1
0.5
0
A1 A2 A3 A4 A6 A7 A8 A10 B1 B2 B4 B5 B7 B8 B9 B10 B11 B13 C3 C5 C6 C7 C8 C10 C12 D3 D5 D6
CLONE 10

FIG.23B

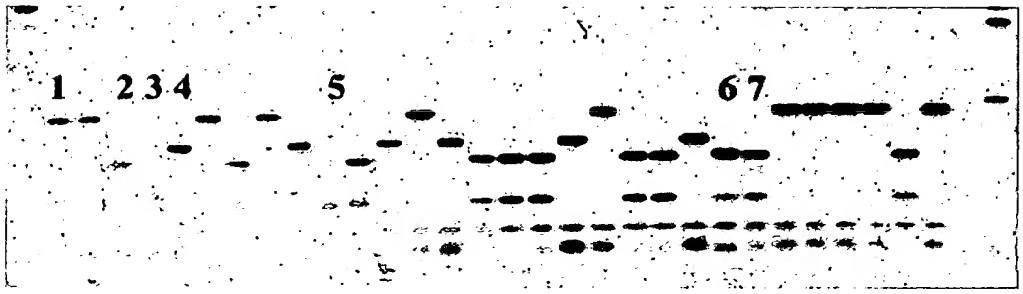


FIG.24

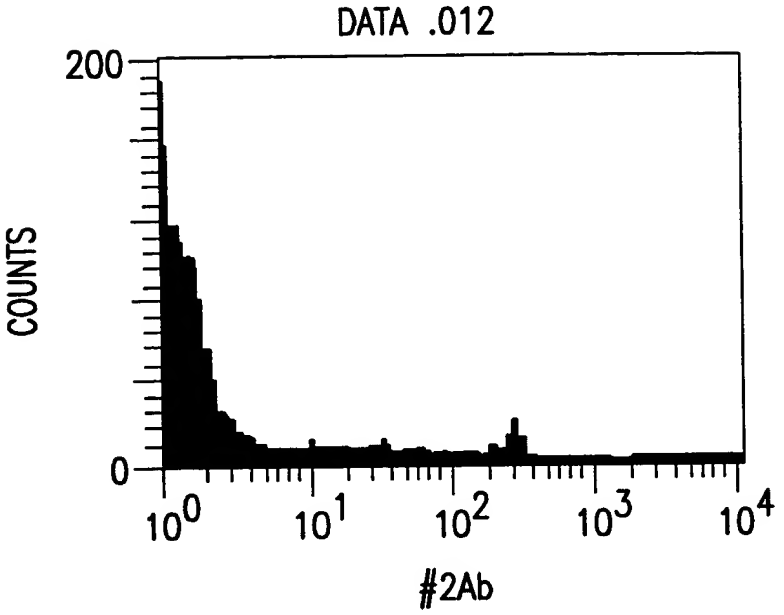


FIG.25A

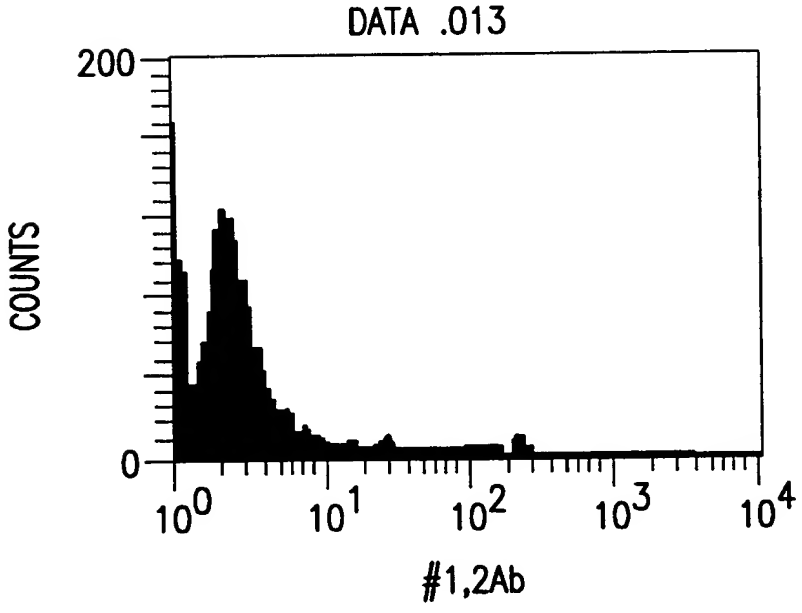


FIG.25B

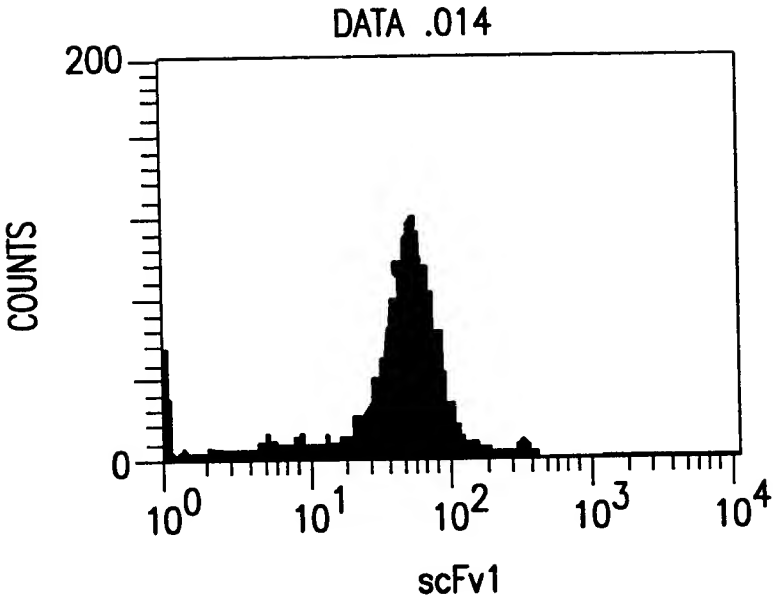


FIG.25C

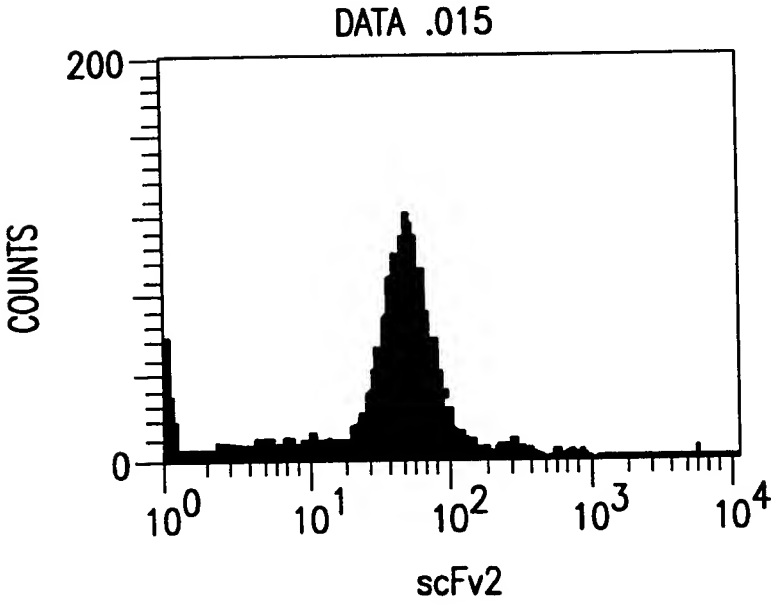


FIG.25D

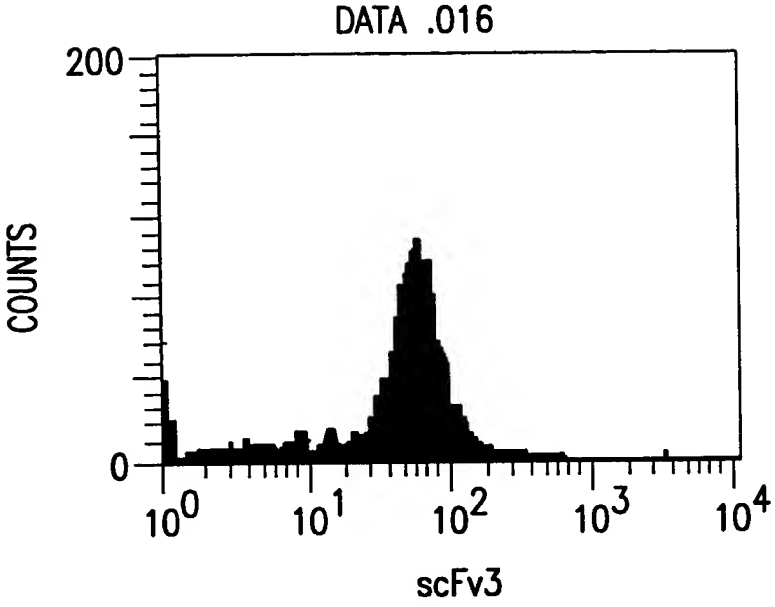


FIG.25E

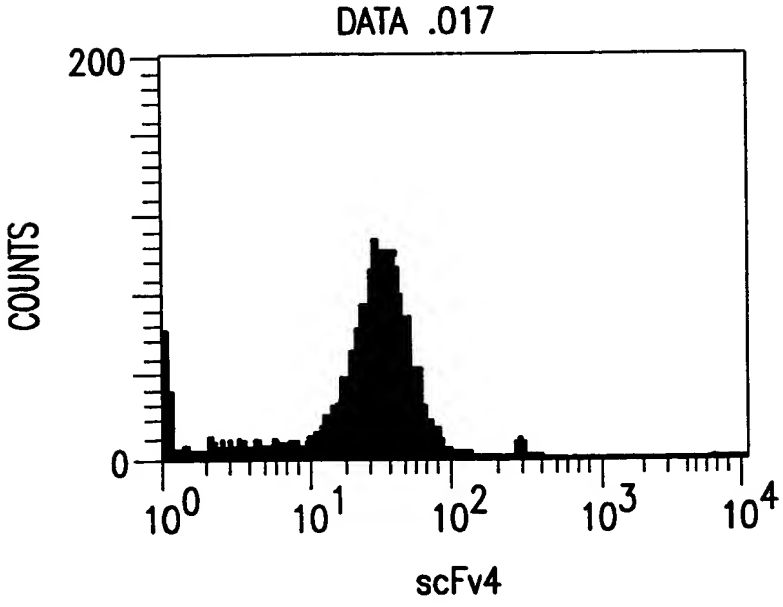


FIG.25F

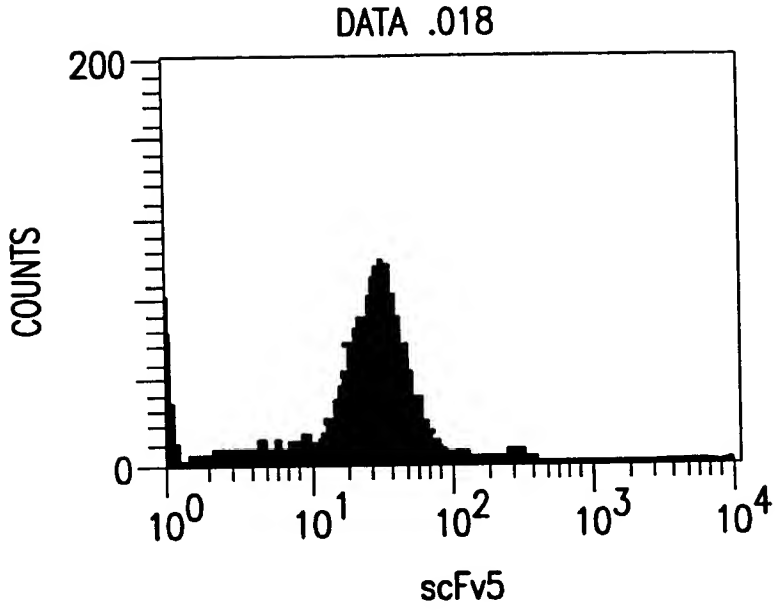


FIG.25G

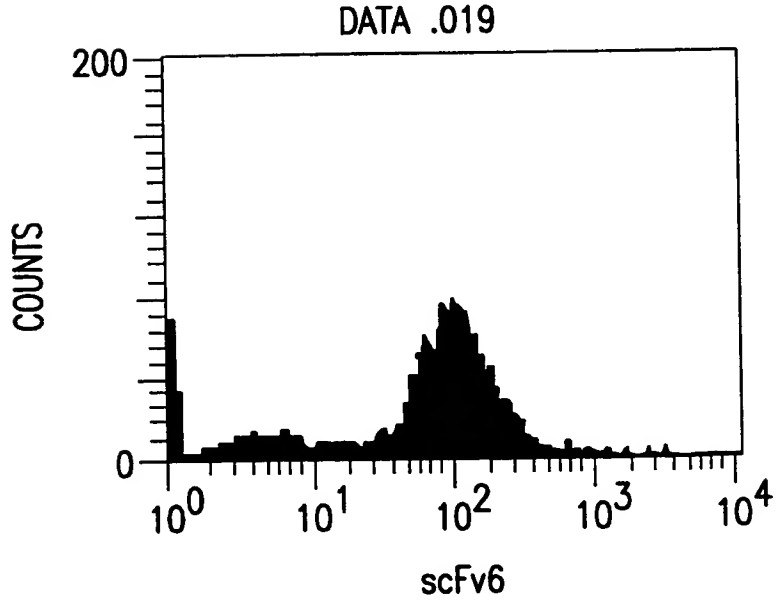


FIG.25H

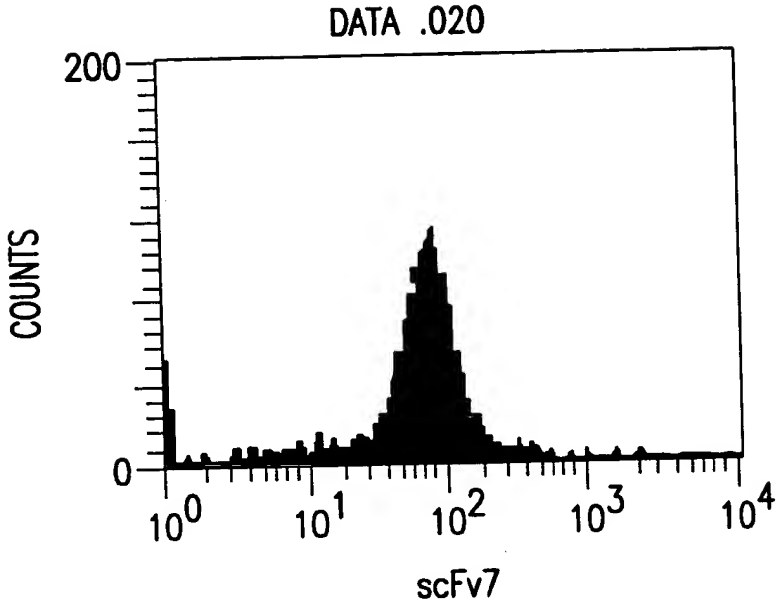


FIG.25I

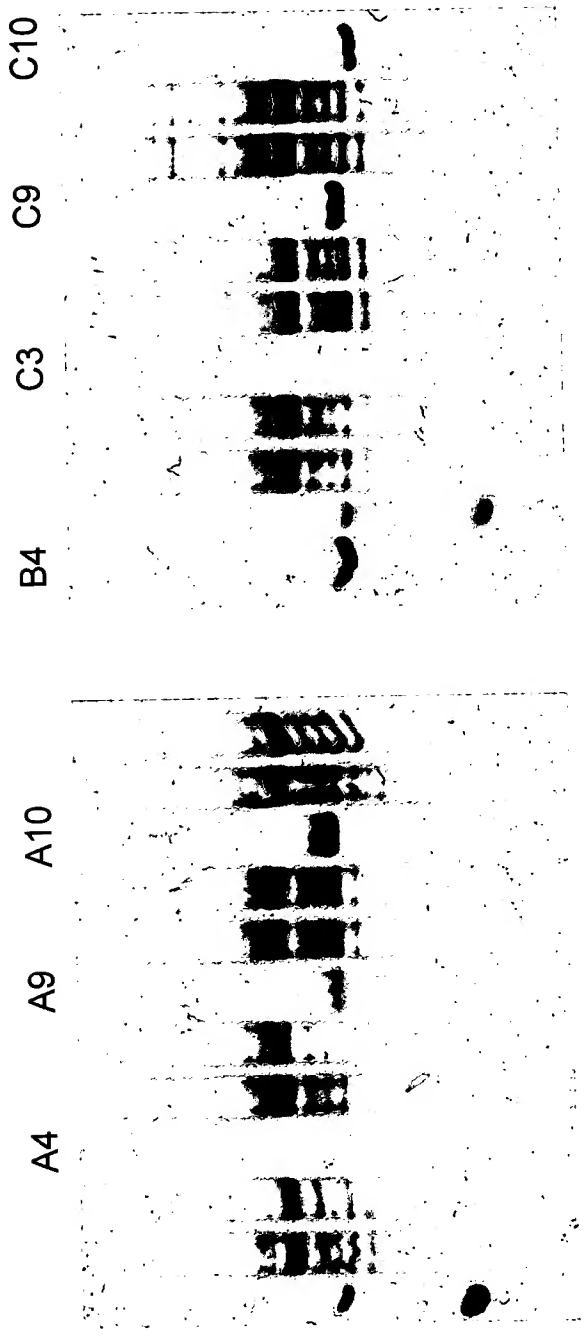


FIG.26

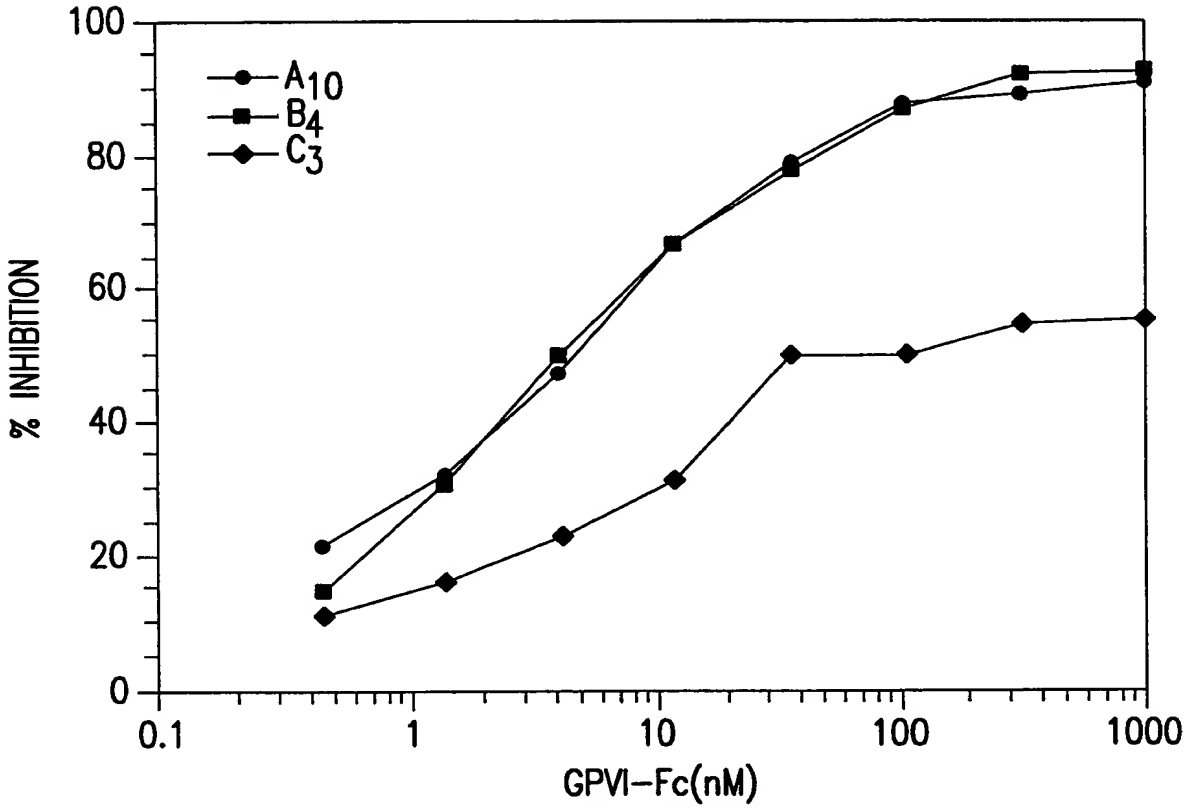


FIG.27